

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 25, 2003, 11:02:53 : Search time 86 Seconds
(without alignments)
6877.365 Million cell updates/sec

Title: US-09-809-545a-1
Perfect score: 1340
Sequence: 1 ggcgcgcgcgcgcgcacacat.....ggcgcgaagggttcgtctaga 1340

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Read size: 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 70 | 5.2 | 2372 | 3 | US-09-145-391-1 |
| 2 | 29 | 2.2 | 1506 | 3 | US-09-176-657-5 |
| 3 | 29 | 2.2 | 1506 | 4 | US-09-421-299-5 |
| 4 | 28 | 2.1 | 1946 | 4 | US-09-620-312D-462 |
| 5 | 27 | 2.0 | 74962 | 4 | US-09-685-853A-3 |
| 6 | 26 | 1.9 | 40 | 3 | US-09-306-290-6 |
| 7 | 26 | 1.9 | 528 | 4 | US-09-542A-12 |
| 8 | 26 | 1.9 | 536 | 1 | US-08-341-568-1 |
| 9 | 26 | 1.9 | 536 | 2 | US-08-911-020-1 |
| 10 | 26 | 1.9 | 631 | 3 | US-09-328-111-361 |
| 11 | 26 | 1.9 | 2481 | 2 | US-08-630-118A-1 |
| 12 | 26 | 1.9 | 2481 | 2 | US-08-838-399-1 |
| 13 | 26 | 1.9 | 2481 | 3 | US-09-235-839-1 |
| 14 | 26 | 1.9 | 2481 | 4 | US-09-327-035-1 |
| 15 | 26 | 1.9 | 2604 | 2 | US-08-630-118A-3 |
| 16 | 26 | 1.9 | 2604 | 2 | US-08-838-399-3 |
| 17 | 26 | 1.9 | 2604 | 3 | US-09-235-839-3 |
| 18 | 26 | 1.9 | 2604 | 4 | US-09-327-035-3 |
| 19 | 26 | 1.9 | 2610 | 4 | US-09-545-814-1 |
| 20 | 26 | 1.9 | 2610 | 4 | US-09-545-814-3 |
| 21 | 26 | 1.9 | 2738 | 2 | US-08-795-868-17 |
| 22 | 26 | 1.9 | 2738 | 4 | US-09-303-069-17 |
| 23 | 26 | 1.9 | 2738 | 4 | US-09-134-250-17 |
| 24 | 26 | 1.9 | 3487 | 4 | US-09-303-069-24 |
| 25 | 26 | 1.9 | 3499 | 4 | US-09-435-376-4 |
| 26 | 26 | 1.9 | 7291 | 4 | US-08-913-942-3 |
| 27 | 25 | 1.9 | 291 | 3 | US-09-329-796-1 |

| | | | | | | |
|----|----|-----|------|---|--------------------|-------------------|
| 28 | 25 | 1.9 | 572 | 4 | US-09-342-653-5 | Sequence 5, Appl1 |
| 29 | 25 | 1.9 | 599 | 4 | US-09-342-647-19 | Sequence 19, Appl |
| 30 | 25 | 1.9 | 608 | 3 | US-09-385-982-183 | Sequence 183, App |
| 31 | 25 | 1.9 | 903 | 5 | PCT-US95-06406A-21 | Sequence 21, Appl |
| 32 | 25 | 1.9 | 1074 | 3 | US-09-357-251-23 | Sequence 23, Appl |
| 33 | 25 | 1.9 | 1126 | 4 | US-09-389-956-7 | Sequence 7, Appl1 |
| 34 | 25 | 1.9 | 1132 | 3 | US-08-894-731-3 | Sequence 3, Appl1 |
| 35 | 25 | 1.9 | 1375 | 4 | US-09-372-422A-37 | Sequence 37, Appl |
| 36 | 25 | 1.9 | 1544 | 2 | US-08-837-593-1 | Sequence 1, Appl1 |
| 37 | 25 | 1.9 | 1584 | 1 | US-08-361-920-24 | Sequence 24, Appl |
| 38 | 25 | 1.9 | 1584 | 1 | US-08-479-939-24 | Sequence 24, Appl |
| 39 | 25 | 1.9 | 1584 | 1 | US-08-483-432-24 | Sequence 24, Appl |
| 40 | 25 | 1.9 | 1932 | 4 | US-09-220-132-143 | Sequence 143, App |
| 41 | 25 | 1.9 | 2071 | 4 | US-09-816-088-1 | Sequence 1, Appl1 |
| 42 | 25 | 1.9 | 2885 | 2 | US-08-791-849A-15 | Sequence 15, Appl |
| 43 | 25 | 1.9 | 2901 | 4 | US-08-368-776A-4 | Sequence 4, Appl1 |
| 44 | 25 | 1.9 | 2901 | 5 | PCT-US96-00419-4 | Sequence 4, Appl1 |
| 45 | 25 | 1.9 | 3008 | 4 | US-09-435-376-6 | Sequence 6, Appl1 |

ALIGNMENTS

```
RESULT 1
US-09-145-391-1
; Sequence 1, Application US/09145391
; Patent No. 6194171
; GENERAL INFORMATION:
; APPLICANT: Puist, Stefan M.
; APPLICANT: Shibata, Hiroki
; TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
; TITLE OF INVENTION: Products Related Thereto and Methods of Using Same
; FILE REFERENCE: CE 3093
; CURRENT APPLICATION NUMBER: US/09/145,391
; CURRENT FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (987)..(1979)
US-09-145-391-1

Query Match      5.2%: Score 70; DB 3; Length 2372;
Best Local Similarity 100.0%: Pred. No. 9.9e-21;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1045 GATGCCAAGACTGAGGAGCCCATGCTGATGATGCGGTCGCTTCTTCATTCAGCAGGCT 1104
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DB      2133 GATGCCAAGACTGAGGAGCCCATGCTGATGATGCGGTCGCTTCTTCATTCAGCAGGCT 2192
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QY      1105 AGTATATACC 1114
        |||||||
DB      2193 AGTATATACC 2202

RESULT 2
US-09-176-657-5
; Sequence 5, Application US/09176657
; Patent No. 6020164
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Aina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/09/176,657
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;; CURRENT FILING DATE: 1998-10-21
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: PERL Program
;; SEQ ID NO 5
;; LENGTH: 1506
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE: -
;; OTHER INFORMATION: 1250374
US-09-176-657-5

Query Match 2.2%; Score 29; DB 3; Length 1506;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 484 ACCGTGTAGAGAGCCGTAATCGAGGT 512
DB 717 ACCGTGTAGAGAGCCGTAATCGAGGT 745

RESULT 3

US-09-421-299-5
; Sequence 5, Application US/09421299
; Patent No. 6524579
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Aime
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/09/421,299
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: 09/176,657
; EARLIER FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1250374
US-09-421-299-5

Query Match

2.2%; Score 29; DB 4; Length 1506;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 484 ACCGTGTAGAGAGCCGTAATCGAGGT 512
DB 717 ACCGTGTAGAGAGCCGTAATCGAGGT 745

RESULT 4

US-09-620-312D-462/C
; Sequence 462, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Peiyan
; APPLICANT: Chen, Ruihong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping

;; APPLICANT: Ma, Yundqing
;; APPLICANT: Wang, Dunrui
;; APPLICANT: Wang, Zhiwei
;; APPLICANT: John Tillinghast
;; APPLICANT: Drmanac, Radoje T.
;; TITLE OF INVENTION: NO. 6569662el Nucleic Acids and
;; FILE REFERENCE: 784CIP2B Polypeptides
;; CURRENT APPLICATION NUMBER: US/09/620,312D
;; CURRENT FILING DATE: 2000-07-19
;; PRIOR APPLICATION NUMBER: 09/552,317
;; PRIOR FILING DATE: 2000-04-25
;; PRIOR APPLICATION NUMBER: 09/488,725
;; PRIOR FILING DATE: 2000-01-21
;; NUMBER OF SEQ ID NOS: 1105
;; SOFTWARE: perl_genes Version 1.0
;; SEQ ID NO 462
;; LENGTH: 1946
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (13)..(1404)
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)..(1946)
;; OTHER INFORMATION: n = a,t,c or g
US-09-620-312D-462

Query Match 2.1%; Score 28; DB 4; Length 1946;
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1172 CAAAAACAAACAAACAAACAAAC 1199
DB 1609 CAAAAACAAACAAACAAACAAAC 1582

RESULT 5

US-09-685-853A-3/C
; Sequence 3, Application US/09685853A
; Patent No. 6479270
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
; FILE REFERENCE: CLO00871 AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/685,853A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/182,194
; PRIOR FILING DATE: 2000-02-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 74962
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(74962)
; OTHER INFORMATION: n = A,T,C or G
US-09-685-853A-3

Query Match 2.0%; Score 27; DB 4; Length 74962;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1289 CAACGAAAAAAAAAAAAAAAAAAAA 1315
DB 28548 CAACGAAAAAAAAAAAAAAAAAAAA 28522

RESULT 6
US-09-306-290-6/c
; Sequence 6, Application US/09306290
; Patent No. 6221635
; GENERAL INFORMATION:
; APPLICANT: Rovera, Giovanni
; TITLE OF INVENTION: METHODS FOR SOLID-PHASE AMPLIFICATION OF DNA TEMPLATE
; FILE REFERENCE: 09924-10
; CURRENT APPLICATION NUMBER: US/09/306,290
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer RGP
US-09-306-290-6

Query Match 1.9%; Score 26; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1288 ACAACGAAAAAAAAAAAAAAAAAAAA 1313
Db 26 ACAACGAAAAAAAAAAAAAAAAAAAA 1

RESULT 7
US-09-105-542A-12
; Sequence 12, Application US/09105542A
; Patent No. 6323329
; GENERAL INFORMATION:
; APPLICANT: Bullerdiek, Jörn
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES OF GENES OF THE
; FILE REFERENCE: BOEHA, 001C1CP
; CURRENT APPLICATION NUMBER: US/09/105,542A
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: PCT/DE96/02494
; PRIOR FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(528)
; OTHER INFORMATION: n = A,T,C or G
US-09-105-542A-12

Query Match 1.9%; Score 26; DB 4; Length 528;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1290 AACGAAAAAAAAAAAAAAAAAAAA 1315
Db 472 AACGAAAAAAAAAAAAAAAAAAAA 497

RESULT 8
US-08-341-568-1
; Sequence 1, Application US/08341568
; Patent No. 5661021
; GENERAL INFORMATION:
; APPLICANT: Buchert, Johanna
; APPLICANT: Silka-aho, Matti

APPLICANT: Viikari, Liisa
APPLICANT: Penttilä, Merja
APPLICANT: Saloheimo, Anu
APPLICANT: Marjatta, Ranna
TITLE OF INVENTION: Mannanase enzymes, genes coding for them,
TITLE OF INVENTION: methods for isolating the genes, and methods for bleaching
TITLE OF INVENTION: pulps
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch and Birch
STREET: PO Box 747
CITY: Falls Church
STATE: VA
COUNTRY: US
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/341,568
FILING DATE: 22-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr, Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 365-262P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: OM9414
US-08-341-568-1

Query Match 1.9%; Score 26; DB 1; Length 536;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1290 AACGAAAAAAAAAAAAAAAAAAAA 1315
Db 460 AACGAAAAAAAAAAAAAAAAAAAA 485

RESULT 9
US-08-911-020-1
; Sequence 1, Application US/08911020
; Patent No. 5854047
; GENERAL INFORMATION:
; APPLICANT: Buchert, Johanna
; APPLICANT: Silka-aho, Matti
; APPLICANT: Viikari, Liisa
; APPLICANT: Penttilä, Merja
; APPLICANT: Saloheimo, Anu
; APPLICANT: Marjatta, Ranna
TITLE OF INVENTION: Mannanase enzymes, genes coding for them,
TITLE OF INVENTION: methods for isolating the genes, and methods for bleaching
TITLE OF INVENTION: lignocellulosic pulps
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch and Birch
STREET: PO Box 747
CITY: Falls Church
STATE: VA

COUNTRY: US
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911.020
FILING DATE: 13-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/341,568
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr, Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 365-262P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORGANISM SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: QM9414
US-08-911-020-1

Query Match 1.9%; Score 26; DB 2; Length 536;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1290 AACGAAAAAAAAAAAAAAAAAAAA 1315
|||||
DB 460 AACGAAAAAAAAAAAAAAAAAAAA 485

RESULT 10
US-09-328-111-361/c
Sequence 361, Application US/09328111
Patent No. 6262333
GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Dertl, Adnan
APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328.111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 361
LENGTH: 631
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(631)
OTHER INFORMATION: n - A,T,C or G
US-09-328-111-361

Query Match 1.9%; Score 26; DB 3; Length 631;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1290 AACGAAAAAAAAAAAAAAAAAAAA 1315
|||||
DB 44 AACGAAAAAAAAAAAAAAAAAAAA 19

RESULT 11
US-08-630-118A-1
Sequence 1, Application US/08630118A
Patent No. 591901
GENERAL INFORMATION:
APPLICANT: Hu Ph.D., Yingshe
APPLICANT: McCaleb Ph.D., Michael L.
APPLICANT: Bloomquist Ph.D., Brian T.
APPLICANT: Flores-Riveros Ph.D., Jaime R.
APPLICANT: Cornfield Ph.D., Linda J.
TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630.118A
FILING DATE: April 8, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield Ph.D., Michael S.
REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 96,149/WH 405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1000
TELEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2481 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 248..1582
US-08-630-118A-1

Query Match 1.9%; Score 26; DB 2; Length 2481;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1290 AACGAAAAAAAAAAAAAAAAAAAA 1315
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DB 2415 AACGAAAAAAAAAAAAAAAAAAAA 2440

RESULT 12
US-08-838-399-1
; Sequence 1, Application US/08838399
; Patent No. 5965392
; GENERAL INFORMATION:
; APPLICANT: Hu Ph.D., Yinghe
; APPLICANT: McCalieb Ph.D., Michael L.
; APPLICANT: Bloomquist Ph.D., Brian T.
; APPLICANT: Flores-Riveros Ph.D., Jaime R.
; APPLICANT: Cornfield Ph.D., Linda J.
; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,399
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenfield Ph.D., Michael S.
; REGISTRATION NUMBER: 37,147
; REFERENCE/DOCKET NUMBER: 96,149/WH 405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)715-1000
; TELEFAX: (312)715-1234
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2481 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 248..1585
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 248..1582
; US-08-838-399-1

Query Match 1.9%; Score 26; DB 2; Length 2481;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1290 AACGAAAAAAAAAAAAAAAAAAAA 1315
Db 2415 AACGAAAAAAAAAAAAAAAAAAAA 2440

RESULT 13
US-09-235-839-1
; Sequence 1, Application US/09235839
; Patent No. 6207799
; GENERAL INFORMATION:
; APPLICANT: Hu Ph.D., Yinghe
; APPLICANT: McCalieb Ph.D., Michael L.
; APPLICANT: Bloomquist Ph.D., Brian T.
; APPLICANT: Flores-Riveros Ph.D., Jaime R.
; APPLICANT: Cornfield Ph.D., Linda J.

; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/235,839
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,118
; FILING DATE: April 8, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenfield Ph.D., Michael S.
; REGISTRATION NUMBER: 37,142
; REFERENCE/DOCKET NUMBER: 96,149-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)913-0001
; TELEFAX: (312)913-0002
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2481 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 248..1582
; US-09-235-839-1

Query Match 1.9%; Score 26; DB 3; Length 2481;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1290 AACGAAAAAAAAAAAAAAAAAAAA 1315
Db 2415 AACGAAAAAAAAAAAAAAAAAAAA 2440

RESULT 14
US-09-327-035-1
; Sequence 1, Application US/09327035
; Patent No. 6368824
; GENERAL INFORMATION:
; APPLICANT: Hu Ph.D., Yinghe
; APPLICANT: McCalieb Ph.D., Michael L.
; APPLICANT: Bloomquist Ph.D., Brian T.
; APPLICANT: Flores-Riveros Ph.D., Jaime R.
; APPLICANT: Cornfield Ph.D., Linda J.
; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/327.035
FILING DATE: 07-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/838,399
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield Ph.D., Michael S.
REGISTRATION NUMBER: 37,147
REFERENCE/DOCKET NUMBER: 96,149/WH 405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1000
TELEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2481 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 248..1585
NAME/KEY: mat_peptide
LOCATION: 248..1582
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-327-035-1

Query Match 1.9%; Score 26; DB 4; Length 2481;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1290 AACGAAAAAAAAAAAAAAAAAAAA 1315
DB 2415 AACGAAAAAAAAAAAAAAAAAAAA 2440

RESULT 15
US-08-630-118A-3
Sequence 3, Application US/08630118A
Patent No. 5919901
GENERAL INFORMATION:
APPLICANT: Hu Ph.D., Yinghe
APPLICANT: McCalieb Ph.D., Michael L.
APPLICANT: Bloomquist Ph.D., Brian T.
APPLICANT: Flores-Riveros Ph.D., Jaime R.
APPLICANT: Cornfield Ph.D., Linda J.
TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,118A
FILING DATE: April 8, 1996

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield Ph.D., Michael S.
REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 96,149/WH 405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1000
TELEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2604 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 371..1705
US-08-630-118A-3

Query Match 1.9%; Score 26; DB 2; Length 2604;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1290 AACGAAAAAAAAAAAAAAAAAAAA 1315
DB 2538 AACGAAAAAAAAAAAAAAAAAAAA 2563

Search completed: September 25, 2003, 11:41:02
Job time : 88 secs

OY 1045 GATGCCAGACTAGAGCCATGATGATGCTCTGTTCTTCT 1092
|||||
DB 13 GATGCCAGACTAGAGCCATGCTGATGATGCTCTGTTCTTCT 60

RESULT 4
US-09-864-761-28375
; Sequence 28375, Application US/09864761
; Patent No. US20020048763A1
GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecomica-X-1
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 28375
LENGTH: 125
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC006075.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.48
OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 0.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.57
OTHER INFORMATION: EST HUMAN HIT: 225303.1, EVALUE 9.00e-61
OTHER INFORMATION: NT HIT: g11431054, EVALUE 2.00e-64
OTHER INFORMATION: SWISSPROT HIT: P54537, EVALUE 1.40e+00
US-09-864-761-28375

Query Match 2.4%; Score 32; DB 9; Length 125;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 247 GGCCAGCCCCAGACACACTTGTGAAAAACAC 278
|||||
DB 9 GGCCAGCCCCAGACACACTTGTGAAAAACAC 40
RESULT 5
US-09-864-761-11804
; Sequence 11804, Application US/09864761
; Patent No. US20020048763A1
GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
FILE REFERENCE: Aecomica-X-1
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 11804
LENGTH: 473
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC006075.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.48
OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 0.5
OTHER INFORMATION: EST HUMAN HIT: 225303.1, EVALUE 9.00e-61
OTHER INFORMATION: NT HIT: g11431054, EVALUE 2.00e-64
OTHER INFORMATION: SWISSPROT HIT: P54537, EVALUE 1.40e+00
US-09-864-761-11804

Query Match 2.4%; Score 32; DB 9; Length 473;
Best Local Similarity 100.0%; Pred. No. 8.8e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 247 GGCCAGCCCGACACACCTTCTGAAACAC 278
DB 296 GGCCAGCCCGACACACCTTCTGAAACAC 327

RESULT 6
US-09-925-302-42
Sequence 42, Application US/09925302
Patent No. US2002004941A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 42
LENGTH: 1574
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1029)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (1076)
OTHER INFORMATION: n equals a,t,g, or c
LOCATION: (1574)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-42

Query Match 2.2%; Score 30; DB 9; Length 1574;
Best Local Similarity 100.0%; Pred. No. 7.6e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1286 AAACAACGAAAAAAAAAAAAAAAAAAAA 1315
DB 1534 AAACAACGAAAAAAAAAAAAAAAAAAAA 1563

RESULT 7
US-10-311-455-1913/C
Sequence 1913, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining the Methylation Status of Genes
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1913
LENGTH: 5898

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1913

Query Match 2.2%; Score 30; DB 12; Length 5898;
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1286 AAACAACGAAAAAAAAAAAAAAAAAAAA 1315
DB 2026 AAACAACGAAAAAAAAAAAAAAAAAAAA 1997

RESULT 8
US-10-240-453-203/C
Sequence 203, Application US/10240453
Publication No. US20030148326A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
TITLE OF INVENTION: by Means of Assessing the Methylation Status of Genes Associated with DNA
FILE REFERENCE: 5013.1009
CURRENT APPLICATION NUMBER: US/10/240,453
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: PCT/EP01/03973
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 350
SEQ ID NO 203
LENGTH: 5898
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-453-203

Query Match 2.2%; Score 30; DB 12; Length 5898;
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1286 AAACAACGAAAAAAAAAAAAAAAAAAAA 1315
DB 2026 AAACAACGAAAAAAAAAAAAAAAAAAAA 1997

RESULT 9
US-10-239-676-179/C
Sequence 179, Application US/10239676
Publication No. US20030082609A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019173.8

```
DE 10032529.7
DE 10043826.1
PRIOR FILING DATE: 2001-04-06
2000-04-06
2000-04-07
2000-06-30
2000-09-01
NUMBER OF SEQ ID NOS: 228
SEQ ID NO 179
LENGTH: 5898
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-239-676-179
```

```
Query Match
Best Local Similarity 100.0%; Score 30; DB 14; Length 5898;
Pred. No. 7.9e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
1286 AACCAACGAAAAAAAAAAAAAAAAAAAA 1315
2026 AACCAACGAAAAAAAAAAAAAAAAAAAA 1997
```

RESULT 10

```
US-10-311-455-1804/C
Sequence 1804, Application US/10311455
Publication No. US2003013606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
PRIOR FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1804
LENGTH: 6126
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1804
```

```
Query Match
Best Local Similarity 100.0%; Score 30; DB 12; Length 6126;
Pred. No. 7.9e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
1286 AACCAACGAAAAAAAAAAAAAAAAAAAA 1315
766 AACCAACGAAAAAAAAAAAAAAAAAAAA 737
```

RESULT 11

```
US-10-311-455-1278/C
Sequence 1278, Application US/10311455
Publication No. US2003013606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
FILE REFERENCE: 5013.1014
```

```
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1278
LENGTH: 6154
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1278
```

```
Query Match
Best Local Similarity 100.0%; Score 30; DB 12; Length 6154;
Pred. No. 7.9e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
1286 AACCAACGAAAAAAAAAAAAAAAAAAAA 1315
882 AACCAACGAAAAAAAAAAAAAAAAAAAA 853
```

RESULT 12

```
US-10-311-455-367/C
Sequence 367, Application US/10311455
Publication No. US2003013606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
PRIOR FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 367
LENGTH: 6510
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-367
```

```
Query Match
Best Local Similarity 100.0%; Score 30; DB 12; Length 6510;
Pred. No. 7.9e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
1286 AACCAACGAAAAAAAAAAAAAAAAAAAA 1315
5115 AACCAACGAAAAAAAAAAAAAAAAAAAA 5086
```

RESULT 13

```
US-10-027-632-174763
Sequence 174763, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Many, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
```

```
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174763
; LENGTH: 2940917
; TYPE: DNA
; ORGANISM: Human
FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2940917)
; OTHER INFORMATION: n = A,T,C or G
US-10-02-632-174763
```

```
Query Match          2.2%; Score 30; DB 13; Length 2940917;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1286 AACACACGAAAAAAAAAAAAAAAAAAAA 1315
DB 2677001 AACACACGAAAAAAAAAAAAAAAAAAAA 2677030
```

```
RESULT 14
US-10-359-385-5
; Sequence 5, Application US/10359385
; Publication No. US20030143622A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Alina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/10/359,385
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/176,657
; PRIOR FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 1250374
US-10-359-385-5
```

```
Query Match          2.2%; Score 29; DB 12; Length 1506;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 484 ACCGTGTAGAGGCGCTAAATCGAGT 512
DB 717 ACCGTGTAGAGGCGCTAAATCGAGT 745
```

```
RESULT 15
US-10-311-455-2039/c
```

```
; Sequence 2039, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Det
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 2039
; LENGTH: 4274
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-2039
```

```
Query Match          2.2%; Score 29; DB 12; Length 4274;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1290 AACGAAAAAAAAAAAAAAAAAAAAATTA 1318
DB 2102 AACGAAAAAAAAAAAAAAAAAAAAATTA 2074
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Search completed: September 25, 2003, 11:46:48
Job time : 334 secs
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352 CAATGTTGGCAATTTGGTAAATATATAGATGTTGAATATATTTTAAATGAGCGGCG 411
1389 CAATGTTGGCAATTTGGTAAATATATAGATGTTGAATATATTTTAAATGAGCGGCG 1448
412 TCGAAGGATTTGTTTGTACCTTTCGAAATATGTCGGATCGGACAGGCGAGAG 471
1449 TCAAAAGGATTTGTTTGTACCTTTCGAAATATGTCGGATCGGACAGGCGAGAG 1508
472 AAATGACAGGATCGGATGAGGCGGTTAAATGAGGATTAATATGACAGCAGC 531
1509 AAATTTACAGGACCGGATGAGGCGGTTAAATGAGGATTAATATGACAGCAGC 1568
532 GTGATGACTAATAAAAAGCGGTGAACCCCTACAGGAATGCGTGAATTAATCACTT 591
1569 GTAATGACAAATAAAAAGCGGTGAACCCCTAATGATGCGTGAATTAATCACTT 1628
592 GTGGGCGGCTCTACAGCCCGGACTTCTATGAGGACGCGTCTTGTCCAGCCAC 651
1629 GTGGGCGGCTCTACAGCTCCGAAATCTATGAGGACGCGTCTTGTCCAGCCAC 1688
652 CAGAGGAGATCTTCATGATGAGTGGCCAGTTAGTTGATATATCTTGTCAATGCTT 711
1689 CAGAGGAGATCTTCATGATGAGTGGCCAGTTAGTTGATATATCTTGTCAATGCTT 1748
712 GCGTTTCAATATCCGCGCCCACTGCTGACGCTGATACCGAGGCGCTACCTTCGAGG 771
1749 GCGTTTCCGTTATCCAGCAGCAGCCCGCGGCGCTACCGAGGCGCGCTGAGAGG 1808
772 GCGTTTCCGTTATCCAGCAGCAGCCCGCGGCGCTACCGAGGCGCGCTGAGAGG 831
1809 GCGTTTCCGTTATCCAGCAGCAGCCCGCGGCGCTACCGAGGCGCGCTGAGAGG 1868
832 TATGCGGAGTATGATATCAAGAGCAGTATGAGCAATTAATGCTACAGGTTGTTAC 891
1869 TACGCGGAGTATGATATCAAGAGCAGTATGAGCAATTAATGCTACAGGTTGTTAC 1926
892 GCTGATACCGCTACGCGCCAGCCCGCTGCTGCTGCTACAGTGA----- 944
1927 GCTGATACCGCTACGCGCCAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1986
945 -----CAGTTACGAGGAG 958
1987 CAGTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2046
959 TTTATGCTGCGAGCCCTACCAACACACACTGCTCAAGCCCACTACGCGCTTGGTG 1018
2047 TTTATGCTGCGAGCCCTACCAACACACACTGCTCAAGCCCACTACGCGCTTGGTG 2106
1019 CCATGATGCTTTTGGCGCTTGAACCATGCGAAGACTAGAGCCATGCTGATGATG 1078
2107 CCATGATGCTTTTGGCGCTTGAACCATGCGAAGACTAGAGCCATGCTGATGATG 2166
1079 GTCGCTGCTTTCTTCAATTTGAGGCTAGTATATACCAAGGAGGATACCAAGCTTGGTC 1138
2167 GTCGCTGCTTTCTTCAATTTGAGGCTAGTATATACCAAGGAGGATACCAAGCTTGGTC 2226
1139 CATATTAATGATAAACCATTTAAACAAACAAACAAACAAACAAACAAACAAAC 1198
2227 CATATTAATGATAAACCATTTAAACAAACAAACAAACAAACAAACAAACAAAC 2250
1199 CAACCTTCCATTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1258
2231 -AACCTTCCATTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2309
1259 GTAGACATCACTTTAGCACTCAAGAAACAAACAAACAAACAAACAAACAAACAA 1318
2310 GTAGACATCACTTTAGCACTTTTAAAAAATGCAAAAAAATGCAAAAAAATGCA 2369

Patent No. 6020164
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Lu, Aina
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
FILE REFERENCE: PF-0611 US
CURRENT APPLICATION NUMBER: US/09/176,657
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PERL Program
SEQ ID NO 5
LENGTH: 1506
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: 1250374
US-09-176-657-5
Query Match 20.6%; Score 275.6; DB 3; Length 1506;
Best Local Similarity 60.2%; Pred. No. 1.5e-68;
Matches 601; Conservative 0; Mismatches 354; Indels 43; Gaps 7;
222 GACAGATGATCCCGCCCGACGAGCGGCGAGC---CCGAGACAGAACCTTGTGAACAC 278
452 GACAGAGGTGAGACACAGACAGAGCGGCGAGAGACAGACACAAATAGTGAATATTC 511
279 AGAAACAAAGTCCAGCCCAAGCGGCTGATGTCCAAATCCCTTCGCTCGGGA 338
512 AGAGAGTAAATCTACCCGAAACGCGTCAATGCTCAATATTCCTTCGCTCCGGA 571
339 TCCAGACCTCCGACAAATGTTTGGCAATTTGTTAAATATATGATGTTGAATATTT 398
572 CCTGACCTCCGCGAGATGTTTGGGAGATTTGGCAATTCCTAGATGAGAAATATCTT 631
399 TAATGAGCGGCTGCGAAGGATTTGTTGTTAATCTTTCGAAATAGTGGATGCGGA 458
632 TAATGAGCGGCTGCGAAGGATTTGTTGTTAATCTTTCGAAATAGTGGATGCGGA 491
459 CAGGCGGAGGAGAAATTTGCAACGATGCTGTAGAGGCGGTTAAATGAGGTTAATA 518
632 CAGGCGGAGGAGAAATTTGCAACGATGCTGTAGAGGCGGTTAAATGAGGTTAATA 751
519 TCGACAGCAGCGGATGATTAATTAAGGCGTGAACCCCTACACCAATGCTGGAA 578
752 TCGTACAGCAGGATTAATGACCAATTAAGGCGTGAACCCCTACACCAATGCTGGAA 811
579 ATTAATCACTTTGCGGCGGCTGCTACAGCCCGGCTGCTGCTGCTGCTGCTGCTGCT 628
812 ATTAATCACTTTGCGGCGGCTGCTACAGCCCGGCTGCTGCTGCTGCTGCTGCTGCT 871
629 CCGGCTGCTTGTGCGAGGCGCAACGAGGATGCTTCATGTA--CAATGGCCCAAGTTC 686
872 AGCAGATGCTGCTGCGAGCAATGATGACAGAGTGCCTTATCAGGAAGAGGCGATCAA 931
687 ACTGTATATCTTCTGCAATGCTGCGGCTTTCATA--TCGGCGGCGGCTGCTGAGC 743
932 CACTTACATTCCTTTAATCATTCCTGCGGCTTCCCTTACCTTACGAGCAGCAGCGAG 991
744 TGCATACGAGGCGCTCACTTTCGAGCGGCTGCTGCGACCGTGTACCAACACTTCAGAG 803
992 CGCTTTCAGAGAGCGCATTTGAGGCGGAGAGGCGGAGACATATATGCTGAGTCCGA 1049
804 TCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 863
1050 -GCGGTACTCTCAAGGCAATCCCGCTATTCAGGCGGCGGCGGCGGCGGCGGCGGCG 1104
864 TGGCAATTAATTTGCTACAGGCTGATACGCTACGAGCGGCGGCGGCGGCGGCGGCG 923
1105 -----ATATGCAAGCGCTGCTACTGCAACCGAGCGGCGGCGGCGGCGGCGGCG 1149

```

QY 924 CACTGCTGCTGCTACAGTACAGTATGAGGAGGATTATGTCGCGACCCCTACACCA 983
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1150 CGGTGACGCGGCTTACAGTACAGTATGAGGAGGATTATGTCGCGACCCCTACACCA 1209
QY 984 CACACTTGTCTGACGCGCGCCACCTACAGGCGGTGGTGCATGATGCTTTTGGCGCTTGAC 1043
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1210 C---CTTGCCCTGCGCTGCTATGAGGAGGATTGCGCGCTGCTGCGAGTTTATACGAGGTG 1266
QY 1044 CGATGCCAGACAGAGGAGGATGCTGATGATGAGGAGGCTGCTTCTTCTTCTTCTTCTTCA 1103
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1267 CTACAGCGCGATTTGCGCGCTGCTGAGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1326
QY 1104 TAGTATATACCAAGGAGGAGGATACACCGTTTGTCTCATTTTAAATGATTAACCATTTAA 1163
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1327 CACTTCTATGAGGCGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1386
QY 1164 CAACACAGCAAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAA 1201
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1387 AGAGGAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAA 1424

```

RESULT 3

```

US-09-421-299-5
: Sequence 5, Application US/09421299
: Patent No. 6524579
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Tang, Y. Tom
: APPLICANT: Corley, Neil J.
: APPLICANT: Guebler, Karl J.
: APPLICANT: Lu, Alina
: APPLICANT: Baughn, Mariah R.
: TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
: FILE REFERENCE: PR-0611 US
: CURRENT APPLICATION NUMBER: US/09/421, 299
: EARLIER FILING DATE: 1999-10-20
: EARLIER APPLICATION NUMBER: 09/176,657
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PERL Program
: SEQ ID NO 5
: LENGTH: 1506
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE: -
: OTHER INFORMATION: 1250374
US-09-421-299-5

```

Query Match 20.6%; Score 275.6; DB 4; Length 1506;

Best Local Similarity 60.2%; Pred. No. 1,5e-68;

Matches 601; Conservative 0; Mismatches 354; Indels 43; Gaps 7;

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QY 222 GACAGATGATCGCCGCCGACGAGCGCCAGC---CCGACACACAACCTTGTGAACAC 278
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 452 GACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 511
QY 279 AGAAAACAAGTCCAGCGCCCAAGGCGTGCATGTCCTCCACATCCCTCCGCTCCGGGA 338
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 512 AGAGAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 571
QY 339 TCCAGACCTTCGACAAATGTTGGCAATTTGTAATAATTAATTAATTAATTAATTAAT 398
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 572 CCTTGACCTCGGCAATGTTGGCAATTTGCAAAATCTTGATGATGAATTAATCTT 631
QY 399 TAATGAGCGGCGTCAAGAGGATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 458
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 632 TAATGAGCGGCGTCAAGAGGATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 691
QY 459 CAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 518
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 692 CAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 751

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QY 519 TGGCAGACGACGCGGTATGACTAATTAATAAAGCGGTGAGACCCCTACACCAATGGCTGAA 578
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 752 TGGTACAGACGCGGTATGACTAATTAATAAAGCGGTGAGACCCCTACACCAATGGCTGAA 811
QY 579 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 628
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 812 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 871
QY 629 CGGTGCTGTTGTCGCGCGCCGCTGACAGGCGCGGCTGACAGGCGCGGCTGACAGGCGG 686
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 872 AGCAGATGCTGCTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 931
QY 687 ACTTGTATATATCTTCTGCAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 743
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 932 CACTTACATCTCTTATATATATATATATATATATATATATATATATATATATATATAT 991
QY 744 TGCATACGAGGCGGCTACCTTTCGAGGCGGCTGTCGACCGGTGTACAAACCTTTCAGAGC 803
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 992 CGCTTTCAGAGGAGGCGGCTTTCGAGGCGGCTGTCGACCGGTGTACAAACCTTTCAGAGC 1049
QY 804 TGGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 863
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1050 -GCGGTACCTTCACAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1104
QY 864 TGGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 923
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1105 -----ATATGACAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1149
QY 924 CACTGCTGCTGCTACAGTACAGTATGAGGAGGATTATGTCGCGACCCCTACACCA 983
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1150 CGGTGACGCGGCTTACAGTACAGTATGAGGAGGATTATGTCGCGACCCCTACACCA 1209
QY 984 CACACTTGTCTGACGCGCGCCACCTACAGGCGGTGGTGCATGATGCTTTTGGCGCTTGAC 1043
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1210 C---CTTGCCCTGCGCTGCTATGAGGAGGATTGCGCGCTGCTGCGAGTTTATACGAGGTG 1266
QY 1044 CGATGCCAGACAGAGGAGGATGCTGATGATGAGGAGGCTGCTTCTTCTTCTTCTTCTTCA 1103
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1267 CTACAGCGCGATTTGCGCGCTGCTGAGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1326
QY 1104 TAGTATATACCAAGGAGGAGGATACACCGTTTGTCTCATTTTAAATGATTAACCATTTAA 1163
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1327 CACTTCTATGAGGCGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1386
QY 1164 CAACACAGCAAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAA 1201
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1387 AGAGGAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAA 1424

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RESULT 4

```

US-09-014-969-14
: Sequence 14, Application US/09014969
: Patent No. 5965397
: GENERAL INFORMATION:
: APPLICANT: Jacobs, Kenneth
: APPLICANT: McCoy, John M.
: APPLICANT: Lavalley, Edward R.
: APPLICANT: Racle, Lisa A.
: APPLICANT: Merberg, David
: APPLICANT: Treacy, Maurice
: APPLICANT: Spaulding, Vikki
: APPLICANT: Agostino, Michael J.
: TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
: TITLE OF INVENTION: ENCODING THEM
: NUMBER OF SEQUENCES: 32
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genetics Institute, Inc.
: STREET: 87 CambridgePark Drive
: CITY: Cambridge
: STATE: MA
: COUNTRY: U.S.A.
: ZIP: 02140
: COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-014-969-14

Query Match 3.8%; Score 51.4; DB 2; Length 2447;
Best Local Similarity 52.1%; Pred. No. 0.0015;
Matches 112; Conservative 1; Mismatches 102; Indels 0; Gaps 0;
DB 1104 TAGTATATACCAAGGGGATACACCGTTTGTCTCATATTAAATGATAAACCATTTAA 1163
DB 2209 TTGTACTTAAATGTGACAAATTAACCTTTGGAGAGAAAAAARAAAAA 2266
DB 1164 CAACACCAAAAAACAACAAAAAACAACCTTCCAAATGGGAGAGAGG 1223
DB 2269 AAAAAA 2328
DB 1224 AAGCTTCCGAGCGCGGTGTGGACACATGCATGACATCCTTACCACTCAA 1283
DB 2329 AAAAAA 2388
DB 1284 AGAAACAAGAAAAAATATA 1318
DB 2389 AAAAAA 2423

RESULT 5
US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:

APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PT29pt-F18
US-08-232-463-14

Query Match 3.7%; Score 50; DB 1; Length 7218;
Best Local Similarity 7.5%; Pred. No. 0.0007;
Matches 17; Conservative 132; Mismatches 77; Indels 0; Gaps 0;
DB 1106 GTATATACCAAGGGGATACACCGTTTGTCTCATATTAAATGATAAACCATTAACA 1165
DB 1467 GCAAGTACTTAAAGATGAGAAATTTGTACRRRRRRRRRRRRRRRRRRRR 1408
DB 1166 AACAAGCAAAAAACAACAAAAAACAACCTTCCAAATGGGAGAGAGAA 1225
DB 1407 RRR 1348
DB 1226 GCTTCCGAGCGCGAGTGTGGACACATGCATGACATCCTTACCACTCAAAG 1285
DB 1347 RRR 1288
DB 1286 AAACACGAAAAAATAAATAAATAAAGCGCCGAGAGG 1331
DB 1287 RRR 1242

RESULT 6
US-08-628-417-6
Sequence 6, Application US/08628417
Patent No. 5627054
GENERAL INFORMATION:
APPLICANT: GILLESPIE, DAVID
TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
TITLE OF INVENTION: POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
CITY: ABERDEEN PROVING GROUND
STATE: MARYLAND
COUNTRY: USA
ZIP: 21010-5423
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,417
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BIFONTI, ULYSSES J
REGISTRATION NUMBER: 39,908
REFERENCE/DOCKET NUMBER: DAM 398-94
TELECOMMUNICATION INFORMATION:
TELEPHONE: 410-671-1158


```

US-09-271-815-3
; Sequence 3, Application US/09271815
; Patent No. 6297036
; GENERAL INFORMATION:
; APPLICANT: BERGSMAN, DERR
; APPLICANT: SHABON, USMAN
; TITLE OF INVENTION: A YAK-1 RELATED SERINE/THREONINE PROTEIN KINASE-HTLAR33
; FILE REFERENCE: GH-70172-1
; CURRENT APPLICATION NUMBER: US/09/271,815
; CURRENT FILING DATE: 1999-03-18
; EARLIER APPLICATION NUMBER: 09/027,064
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 60/053,924
; EARLIER FILING DATE: 1997-07-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1338
; TYPE: DNA
; ORGANISM: Homo sapiens
-09-271-815-3

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Query Match          3.4%; Score 45.2; DB 3; Length 1338;
Best Local Similarity 47.8%; Pred. No. 0.0062;
Matches 131; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

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QY 3 GGGCGCCCTGACACATGCTCAGCTTATGCTTCGCGAGTTCGCTCCACCCAGAAAT 62
   |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 686 GGTGCGCCCATACACACCTTCACACACCCCGGAGCTGATGATGAGCTGGTG 745
QY 63 GGCATCTCTGACAAATACAGGCGCTCATCCCATTCGCGCGCAGAGACAGCGCCAGCC 122
   |||  |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 746 GCGGCGCTGCTACGCTCTCCACCTGACCGCGCTGCGCCCGCAGCAGCGGCTGCT 805
QY 123 CACTGTCGCCGACACATTAATGATCTCTTACAGACAGCGAGCTGGAGAGAGCG 182
   ||  ||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 806 CAGCCCTCGGAGCTGGATGAGTGTGAGTGTGCTCCACCGCTCCGCTCTGATGACCTG 865
QY 183 CTTATACAGCGCAGACGCGTCTCGGACCGCCAGAGAGAGATGATGCGCCCGAC 242
   ||  ||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 866 CCACTCTGGGGCTGACCTGCGCTCGCTGCTGATGACCGAGAGACAGCAGCAGCTCGTG 925
QY 243 CGACGGCCAGCCCGCAGACACATTTCTTAAC 270
   ||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 926 ACCCTGCCCCCTGCTGCGGCGCCCTGCTGAAGC 959

```

RESULT 10

-09-027-064-1
Sequence 1, Application US/09027064
Patent No. 6133006

```

; GENERAL INFORMATION:
; APPLICANT: SHABON, USMAN
; APPLICANT: BERGSMAN, DERR
; TITLE OF INVENTION: A YAK-1 RELATED SERINE/THREONINE
; TITLE OF INVENTION: PROTEIN KINASE-HTLAR33
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P. O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,064
; FILING DATE: 20-FEB-1998
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/053,924
; FILING DATE: 28-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2394 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-027-064-1

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Query Match          3.4%; Score 45.2; DB 3; Length 2394;
Best Local Similarity 47.8%; Pred. No. 0.0087;
Matches 131; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

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QY 3 GGGCGCCCTGACACATGCTCAGCTTATGCTTCGCGAGTTCGCTCCACCCAGAAAT 62
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DB 1742 GGTGCGCCCATACACACCTTCACACACCCCGGAGCTGATGATGAGCTGGTG 1801
QY 63 GGCATCTCTGACAAATACAGGCGCTCATCCCATTCGCGCGCAGAGACAGCGCCAGCC 122
   |||  |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1802 GCGGCGCTGCTACGCTCTCCACCTGACCGCGCTGCGCCCGCAGCAGCGGCTGCT 1861
QY 123 CACTGTCGCCGACACATTAATGATCTCTTACAGACAGCGAGCTGGAGAGAGCG 182
   ||  ||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1862 CAGCCCTCGGAGCTGGATGAGTGTGAGTGTGCTCCACCGCTCCGCTCTGATGACCTG 1921
QY 183 CTTATACAGCGCAGACGCGTCTCGGACCGCCAGAGAGAGATGATGCGCCCGAC 242
   ||  ||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1922 CCACTCTGGGGCTGACCTGCGCTCGCTGCTGATGACCGAGAGACAGCAGCAGCTCGTG 1981
QY 243 CGACGGCCAGCCCGCAGACACATTTCTTAAC 276
   ||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 1982 ACCCTGCCCCCTGCTGCGGCGCCCTGCTGAAGC 2015

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RESULT 11

US-09-271-815-1
Sequence 1, Application US/09271815
Patent No. 6297036

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; GENERAL INFORMATION:
; APPLICANT: BERGSMAN, DERR
; APPLICANT: SHABON, USMAN
; TITLE OF INVENTION: A YAK-1 RELATED SERINE/THREONINE PROTEIN KINASE-HTLAR33
; FILE REFERENCE: GH-70172-1
; CURRENT APPLICATION NUMBER: US/09/271,815
; CURRENT FILING DATE: 1999-03-18
; EARLIER APPLICATION NUMBER: 09/027,064
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 60/053,924
; EARLIER FILING DATE: 1997-07-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2394
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-271-815-1

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Query Match          3.4%; Score 45.2; DB 3; Length 2394;
Best Local Similarity 47.8%; Pred. No. 0.0087;
Matches 131; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

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QY 3 GGGCGCCCTGACACATGCTCAGCTTATGCTTCGCGAGTTCGCTCCACCCAGAAAT 62

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Db 1742 GGTGTGCTCCATCAACCACTCACCACACCCCGAGCTGATGATGAGCTGTG 1801
QY 63 GGCAATCTCGAGATATACAGSGCCCTCATTCCTCCGCGCCAGACACCAGCC 122
Db 1802 GGGCGCTGCTGACTGCTCCACCTCACAGCGCCCGCCAGACCGCTGCT 1861
QY 123 CACGTGCTCCGCGCACATTAATTAATCTCTACACAGACGACCTGAGAGAGCG 182
Db 1862 CAGCCCTCCGAGCTGAGTACTGAGAGTCTCCACCTCCCTCCCTCTGATGACCTG 1921
QY 183 CTATACAGGACGACAGCGCTCTCCGACCCGACACAGACAGATGAGCGCCGAC 242
Db 1922 CCACTCTGGGGCTCTACCTGCGCTCCGCTGCTACCCAGACAGACGACCTGCTG 1981
QY 243 CGAGCGGCGACCCGACACACACTTCTGAAAAC 276
Db 1982 ACCCTGCCCCCTCCCTGCGGCGCCCTCTGAAAAGC 2015

RESULT 12
S-08-676-967-2
: Sequence 2, Application US/08676967
: Patent No. 5747317
: GENERAL INFORMATION:
: APPLICANT: COLLINS, KATHLEEN
: TITLE OF INVENTION: Human Telomerase
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Science & Technology Law Group
: STREET: 268 Bush Street, Suite 3200
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/676,967
: FILING DATE:
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Osman Ph.D., Richard A
: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: UCB96-055
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415)343-4341
: TELEFAX: (415)343-4342
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2277 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-08-676-967-2

Query Match 3.4%; Score 45; DB 1; Length 2277;
Best Local Similarity 32.4%; Pred. No. 0.0096;
Matches 109; Conservative 46; Mismatches 178; Indels 3; Gaps 1;

QY 215 CCACACAGACAGATGATGCGCCCGACGCGACGCCGACACCAACCTTGTGAAA 274
Db 257 CNAARGAARAAAGNAARAAAGARAAAYWSNGARTGCCNAARAGARCCNAARCCNARA 316
QY 275 ACACAGAAAACAAGTCCCGACGCGCGCTGCTGCTGCTCAACATCCCTCCGGTTC 334
Db 317 ARGCAARAGTNGCAGTAARARARCCNMGNTNATHATHMGAAYTTWMSNTTYAARTGY 376
QY 335 GGGATCCAGACCTCCGACCAATGTTTGGCCAAATTTGTAATAATTTGATGTTGAATTA 394
Db 335 GGGATCCAGACCTCCGACCAATGTTTGGCCAAATTTGTAATAATTTGATGTTGAATTA 394

Db 377 SNGARGAAYGAYTNAARACNCTNTTTCNCARTTYGGGNGCTVYTNARGSTNAAYATHC 436
QY 395 TTTTAA---TGACGGGGGCTCCGAAGGATTTGGTTTCTGTAATTTGCAAAATGTCGG 451
Db 437 CNMGNAARCCGAGGNAARATGNGNTTGGNTTGGTTCATTTAAARAAATYNTYNG 496
QY 452 ATGGGACAGGGCGGAGGAGAAATTTGACGCTGACGCTGAGAGCGCGTAATAATTCAGG 511
Db 497 ARGCGNAARCCATYTNAAARGNATGAAATATGARGARATHAARGMNGNCGTNGCNG 556
QY 512 TTAATTAATGCGACAGACGCGCTGATGACTAATAAAA 547
Db 557 TNGAYTGGCGTNGCNAARGAATATAYARAGAYA 592

RESULT 13
US-08-676-974-2
: Sequence 2, Application US/08676974
: Patent No. 5770422
: GENERAL INFORMATION:
: APPLICANT: COLLINS, KATHLEEN
: TITLE OF INVENTION: Human Telomerase
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Science & Technology Law Group
: STREET: 268 Bush Street, Suite 3200
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/676,974
: FILING DATE:
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Osman Ph.D., Richard A
: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: UCB96-055
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415)343-4341
: TELEFAX: (415)343-4342
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2277 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-08-676-974-2

Query Match 3.4%; Score 45; DB 1; Length 2277;
Best Local Similarity 32.4%; Pred. No. 0.0096;
Matches 109; Conservative 46; Mismatches 178; Indels 3; Gaps 1;

QY 215 CCACACAGACAGATGATGCGCCCGACGCGACGCCGACACCAACCTTGTGAAA 274
Db 257 CNAARGAARAAAGNAARAAATGARAAYWSNGARTGCCNAARAGARCCNARA 316
QY 275 ACACAGAAAACAAGTCCCGACGCGCGCTGCTGCTGCTCAACATCCCTCCGGTTC 334
Db 317 ARGCAARAGTNGCAGTAARARARCCNMGNTNATHATHMGAAYTTWMSNTTYAARTGY 376
QY 335 GGGATCCAGACCTCCGACCAATGTTTGGCCAAATTTGTAATAATTTGATGTTGAATTA 394
Db 377 SNGARGAAYTNAARACNCTNTTTCNCARTTYGGGNGCTVYTNARGSTNAAYATTC 436
QY 395 TTTTAA---TGACGGGGGCTCCGAAGGATTTGGTTTCTGTAATTTGCAAAATGTCGG 451

DB 437 CMMGNAAACGAYGNAAATGATGACGCTTGGTTCATCTTAAATTAATGATG 496
QY 452 ATCCGACAGGCGGAGGAGAAATGACCGCTAGAGCGGCTAAATGAGG 511
DB 497 AAGCGNAAACGCTTAAATGATGATGATGATGATGATGATGATGATGATG 556
QY 512 TTAATTAATGCGACGACGCGCTGATGATGATGATGATGATGATGATGATG 547
DB 557 TNGAYTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 592

RESULT 14
US-09-098-487-2
; Sequence 2, Application US/09098487
; Patent No. 5917025
; GENERAL INFORMATION:
; APPLICANT: COLLINS, Kathleen
; TITLE OF INVENTION: Human Telomerase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/098,487
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman Ph.D., Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UCB96-055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415)343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2277 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-098-487-2

Query Match 3.4%; Score 45; DB 2; Length 2277;
Best Local Similarity 32.4%; Pred. No. 0.0096;
Matches 109; Conservative 46; Mismatches 178; Indels 3; Gaps 1;

QY 215 CCACACAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 274
DB 257 CNAAGARARAGCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 316
QY 275 ACACAGAAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 334
DB 317 AAGCNAARCTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 376
QY 335 GAGATCCAGACCTGACGATGATGATGATGATGATGATGATGATGATGATGATGATG 394
DB 377 SNGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 436
QY 395 TTTTAA--TGAGGCGGCTGCAAGGATGATGATGATGATGATGATGATGATGATG 451
DB 437 CMMGNAAACGCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 496
QY 452 ATCCGACAGGCGGAGGAGAAATGACCGCTGATGATGATGATGATGATGATGATG 511

DB 497 AAGCGNAAACGCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 556
QY 512 TTAATTAATGCGACGACGCGCTGATGATGATGATGATGATGATGATGATGATG 547
DB 557 TNGAYTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 592

RESULT 15
US-09-620-312D-1019
; Sequence 1019, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyun
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhilwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: PL_FL_genes Version 1.0
; SEQ ID NO 1019:
; LENGTH: 1477
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)..(753)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1477)
; OTHER INFORMATION: n = a,t,c or g
US-09-620-312D-1019

Query Match 3.3%; Score 44.8; DB 4; Length 1477;
Best Local Similarity 52.0%; Pred. No. 0.0085;
Matches 128; Conservative 0; Mismatches 112; Indels 6; Gaps 1;

QY 295 CCCAAGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 354
DB 442 CCAATGCGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 501
QY 355 ATGTTGGGCAATTTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 408
DB 502 ACTTTGAGCCCTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 561
QY 409 GCGTCGAGAGGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 468
DB 562 CCGCTTAAGGTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 621
QY 469 GAGAAATGCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 528
DB 622 GAACATGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 681

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| QY | 529 | CGCGTG | 534 |
| | 11 | 11 | |
| Db | 682 | CGACTG | 687 |

Search completed: September 25, 2003, 11:39:25
Job time : 90 secs

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301 CGGCTGCATGTGTCCAAATATCCCTTCCTCCGGTCCGGGATCCAGACTCCGACAAATGTTT 360
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361 GGGCAATTTGGTAAATATATAGATGTGAATTTATTTTAAATAGACGGGGCTCGAAGGA 420
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421 TTTGGTTTCGTAACTTTGGAAAAATAGTGGGATGGGACAGGGGAGGAGGAATTCAC 480
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781 ACCGTGTACAAACACCTTACAGAGCTGGGGGCCGCCCAACCCGCTATATGGCGGA 840
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841 GTAGGTATCAAGAGCCAGTGTATGGCAATTAATTTGCTACAGAGGTGTACCTGCTCATAC 900
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1201 ACCTTCATGTGTGGGAGAGAGAGTTCGAGGCCGAGTGTGTGACATGATGAGT 1260
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1261 AGGACATCACTTTAGCACTCAAAAGAACAGAAAAAATTAATTAATTAATTAATTAATTA 1320
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1321 GGCGCAAGGGGTTCGCTAGA 1340

Db 1321 GGCGCAAGGGGTTCGCTAGA 1340
RESULT 2
US-09-794-591-1
; Sequence 1, Application US/09794591
; Patent No. US20010018198A1
; GENERAL INFORMATION:
; APPLICANT: Pulst, Stefan M.
; APPLICANT: Shibata, Hiroki
; TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
; FILE REFERENCE: CE 3093
; CURRENT APPLICATION NUMBER: US/09/794,591
; PRIOR APPLICATION NUMBER: 09/145,391
; PRIORITY DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (987)..(1979)
US-09-794-591-1
Query Match 64.0%; Score 857.2; DB 9; Length 2372;
Best Local Similarity 82.7%; Pred. No. 6,9e-233;
Matches 1141; Conservative 0; Mismatches 138; Indels 101; Gaps 10;
1 GCGGCGCCGCTGACACATATGCTCAG-CTTATGCTCAGGCGCATTCGCTCACCCGAG 59
1029 GCGGCGCCGCTGACACATATGCTCAG-CTTATGCTCAGGCGCATTCGCTCACCCGAG 1088
60 AATGCAATCTT-GCAGAAATACAGGCGCCCTCATCCCATCCCGCCAGAG-ACACCGCG 117
1089 AAGGTAATCCCGCGGAATACAGGCGCCCTCATCCCATCCCGCCAGAG-ACACCGCG 1148
118 CAGCCCACTGTCGCGG-CCACATTAATTAATTTGCTCCTACACAGAGCTGCGAG 175
1149 CAGCCCACTGTCGCGG-CCACATTAATTAATTTGCTCCTACACAGAGCTGCGAG 1208
176 CAGAGC---GCTTATACAAAGCGCAGAG-CCGCTCCTGCGCAGCGCCACAGACAGATGAT 231
1209 CAGAGC---GCTTATACAAAGCGCAGAG-CCGCTCCTGCGCAGCGCCACAGACAGATGAT 1268
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1269 GCGGCGCCGCTGACACATATGCTCAG-CTTATGCTCAGGCGCATTCGCTCACCCGAG 1328
232 CAGCCCACTGTCGCGG-CCACATTAATTAATTTGCTCCTACACAGAGCTGCGAG 351
1329 CAGCCCACTGTCGCGG-CCACATTAATTAATTTGCTCCTACACAGAGCTGCGAG 1388
352 CAATATGTTGGCAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 411
1389 CAATATGTTGGCAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1448
412 TCGAAGGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 471
1449 TCGAAGGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1508
472 AAATGCAAGGATTCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 531
1509 AAATGCAAGGATTCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1568
532 GTGATGACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 591
1569 GTGATGACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1628

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OY 592 GTGGGCGGCTACAGCCCGGACTTCTATGACAGGCGGTGTGTGTGCCAGGCCAAC 651
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Db 1629 GTGGGTGACGTACAGTCCCGAATCTATGACAGGCGGTCTCTGTGTGCCAGGCCAAC 1688
OY 652 CAGAGGATCTTCCATGTACAGTGGCCCACTTCTATTAATCTTGTGCAGTCCCT 711
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Db 1689 CAGAGGATCTTCCATGTACAGTGGCCCACTTCTATTAATCTTGTGCAGTCCCA 1748
OY 712 GGGCTTCATATCGGCGGCGGCTGTGACAGTGCATACGAGGGGCTGACCTTCGAGGC 771
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1749 GGGCTTCATATCGAGCGGCGGCGGCTGTGACAGGAGGGGCGGCTGTGAGGC 1808
OY 772 CGTGTGCGACCGGTGACAAACACCTTTCAGAGCTGCGGCGGCGGCGGCGGCGGCGG 831
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1809 CGGCGTGCACCGGTGACAAACACCTTTCAGAGCGGCGGCGGCGGCGGCGGCGGCGG 1868
OY 832 TATGGCGAGTACTGTATCAAGAGCGGCTGTATGGCAATTAATGTCTACAGGGTGTAC 891
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Db 1869 TACGGCGGTGTGTATAC--CAGGATGATTTATATGTGTGACAGATTTATGTGTAT 1926
OY 892 GCTGATACCGGTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 944
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1927 GCTGATACCGGTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1986
OY 945 -----CAGTTACGAGAGAG 958
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1987 CAGTTGCTTCTGTTGACAGAGATGAATTTCTTGTATACACTCTGACGTTTACGAGAG 2046
OY 959 TTTATGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1018
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2047 TTTATGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2106
OY 1019 CCAATGAATGTTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1078
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2107 CCAATGAATGTTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2166
OY 1079 GTCCTGCTTCTTCTATTCAGGCGGATATATACCAAGGGGATACCAACCGTTTGTCT 1138
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2167 GTCCTGCTTCTTCTATTCAGGCGGATATATACCAAGGGGATACCAACCGTTTGTCT 2226
OY 1139 CATATTAATGATTAACCACTTAACCAACCAACCAACCAACCAACCAACCAACCAAC 1198
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2227 CATATTAATGATTAACCACTTAACCAACCAACCAACCAACCAACCAACCAACCAAC 2250
OY 1199 CAACCTTCATGTTGGGAGAGAGAACTTTCGAGGCGGCGGCGGCGGCGGCGGCGGCGG 1258
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Db 2251 -AACCTTCATGTTGGGAGAGAACTTTCGAGGCGGCGGCGGCGGCGGCGGCGGCGG 2309
OY 1259 GTAGAGATCATTGTAGCAACTCAAGAAACAGAAACAGAAACAGAAACAGAAACAGAA 1318
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Db 2310 GTAGATCATCTTTTACCAATTTTAAAAAATATCAAAAAAATATCAAAAAAATATCA 2369

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RESULT 3
US-10-359-385-5
; Sequence 5, Application US/10359385
; Publication No. US20030143622A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Aina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/10/359,385
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/176,657
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 5

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; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 1250374
US-10-359-385-5

Query Match
Best Local Similarity 60.28; Pred. No. 1.3e-67;
Matches 601; Conservative 0; Mismatches 354; Indels 43; Gaps 7;

OY 222 GACAGATGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 278
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 452 GACAGAGAGGTGAGACAGACAGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 511
OY 279 AGAAGAGTAAATCAACCCCGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 571
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 512 AGAAGAGTAAATCAACCCCGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 571
OY 339 TCCAGACCTCCGCAAAATGTTTGGCAATTTGTAATAATATTAATTAATTAATTTT 398
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 572 CCTGACCTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 631
OY 399 TAAATGACGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 458
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 632 TAAATGACGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 691
OY 459 CAGGCGGAGGAGAAATGACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 518
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 692 CAGGCGGAGGAGAAATGACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 751
OY 519 TCGGACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 578
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 752 TCGTACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 811
OY 579 ATTAATCAAGTTGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 628
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 812 ATTAATCAAGTTGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 871
OY 629 CGGTGCTGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 686
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 872 AGCAGATGTGCTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 931
OY 687 ACTTGTATATCTTCTGCAATGCGTGTGCTTCTCAATA--TCCGCGCGCGGCGGCGGCGG 743
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 932 CACTTTCATCTTCTTATATCAATTCCTGCTTCCCTTACCTTACGAGCGGCGGCGGCGG 991
OY 744 TGCATACGAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 803
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 992 CGCTTTCAGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1049
OY 804 TGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 863
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1050 -GGGATACCTTCAACAGCCATCCCGGCTTATCCAGGGGATGATATGAGAGGCTTACAG 1104
OY 864 TGGCAATTAATTTCTACAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 923
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1105 -----ATATGACAGCGCTGTACTTCAACCGGCGGCGGCGGCGGCGGCGGCGGCGG 1149
OY 924 CACTGCTGTGCTTACAGTACAGTACAGGAGGATTAATGCTGCGGCGGCGGCGGCGGCGG 983
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1150 CGCTGAGAGCGGCTTACAGTACAGGAGGATTAATGCTGCGGCGGCGGCGGCGGCGGCGG 1209
OY 984 CACACTGTGCTACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1043
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1210 C---CTTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1266
OY 1044 CGATGCGCAAGTACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1103
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1267 CTACAGCGGATTTGCCCGCTTACAGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1326
OY 1104 TACTATATACCAAGGGGATACCAACCTTTGCTCCATATTAATATGAATTAACCATTTAA 1163
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; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 22653
; LENGTH: 224
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006075.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2
; OTHER INFORMATION: NT HTT: g18922072, EVALUATE 1.00e-123
; OTHER INFORMATION: SWISSPROT HIT: Q09457, EVALUATE 8.00e-03
; OTHER INFORMATION: EST_HUMAN HIT: AU118435.1, EVALUATE 1.00e-123
US-09-864-761-22653
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Query Match 6.6%; Score 88; DB 9; Length 224;
Best Local Similarity 82.6%; Pred. No. 9.2e-15;
Matches 185; Conservative 0; Mismatches 30; Indels 9; Gaps 7;
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QY 5 CCGCCCTGACACAAATGGCTCAG-CTTATGCTCAGCGGCGAGCTCCACCCGAGATG 63
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 CTGCCCTGACACAAATGGCTCAGCTTACGCTCGGCCAGTTGCTCCCGGAGAAC 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 64 GCATGCT-GCAGATACAGGCGCCCTCATTCCTCCCGGCGAG-ACACGCGGAC 121
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 GTATCCCGGGAATACAGCGCCCTCATTCCTCCCGGCGAGAGTACAGGCGACA 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 122 CCACTGTCGCG-CCACACATTAACTTG-ATCCTCTACAGACGAGCTCGAGGAGA 179
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 CCACGTTCCCGACACATTAACTTACCTTCCCGGCGAGAGTCTCGAGGAGA 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 180 GC---GCTTATACAGGCGACAG-CCGTTCTCCGCGACGCGACA 219
    || || || || || || || || || || || || || || || || || || ||
DB 181 GCCCGGCGAGACAGCGGCTCAGACCGTCTGTGCGACGCGACA 224
    || || || || || || || || || || || || || || || || || || ||
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RESULT 8
; Sequence 5893, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Acomlca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
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; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 5893
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006075.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
US-09-864-761-5893
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Query Match 6.4%; Score 86.4; DB 9; Length 454;
Best Local Similarity 83.5%; Pred. No. 4e-14;
Matches 157; Conservative 0; Mismatches 26; Indels 5; Gaps 5;
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QY 1 GCGCGCGCCCTGACACAAATGGCTCAG-CTTATGCTCAGCGGCGAGTTGCTCCACCCAG 59
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DB 246 GCCGCTCCCTGACACAAATGGCTCAGCTTACGCTTCGGCGCGAGTTGCTCCCGCAG 305
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 60 AATGCGATGCT-GCAGATACAGGCGCCCTCATTCCTCCCGGCGAGAG-ACACGGG 117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 306 AACGTTATCCCGGGAATACAGGCGCCCTCATTCCTCCCGGCGAGAGTACACAGGC 365
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 118 CAGCCACTGTCGCG-CCACACATTAACTTG-ATCCTCTACAGACGAGCTCGAG 175
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 366 CAGACACAGGTTCCGAGACACATTAACTTACCTTCCCGGCGAGAGCTCGAG 425
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 176 CAGAGCGC 183
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 426 CAGAGCC 433
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RESULT 9
; Sequence 2191, Application US/10017161
; Publication No. US2003014368A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
```


APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABUGATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2191
LENGTH: 2350
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: source
LOCATION: (1)..(2350)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(2150)
FEATURE:
NAME/KEY: modified_base
LOCATION: (2)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (7)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (9)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (13)..(15)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (17)..(18)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (20)..(21)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (23)..(24)
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NAME/KEY: modified_base
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OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified_base
LOCATION: (34)
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FEATURE:
NAME/KEY: modified_base
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NAME/KEY: modified_base
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FEATURE:

NAME/KEY: modified_base
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NAME/KEY: modified_base
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FEATURE:
NAME/KEY: modified_base
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OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified_base
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FEATURE:
NAME/KEY: modified_base
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LOCATION: (170)..(171)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (179)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (195)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (197)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (209)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base

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LOCATION: (212)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (214)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (216)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (218)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (290) ..(291)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (302)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (309)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (315)
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NAME/KEY: modified_base
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NAME/KEY: modified_base
LOCATION: (320)
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FEATURE:
NAME/KEY: modified_base
LOCATION: (323)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (327)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (332)

Query Match 4.3%; Score 58; DB 12; Length 2350;
Best Local Similarity 57.5%; Pred. No. 1.2e-05;
Matches 103; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 1140 ATATTAAATGATTAACCATTTAAACAAACAGCAAAACAAACAAACAAACAAAC 1199
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Db 1130 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1061

QY 1200 AACCTTCCAAATGGGAGAGAGAACTTCCGAGCCCGAGTGTGGACACATGCGAG 1259
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1060 AAAAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1001

QY 1260 TAGGACATCACTTTAGCAACTCAAGAAACGAAAAAATATAA 1318
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1000 AGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942

RESULT 10
US-09-908-975-27923
; Sequence 27923, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, AVI
```

```
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Liat
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLI
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 27923
LENGTH: 65
TYPE: DNA
ORGANISM: Mus musculus
US-09-908-975-27923

Query Match 4.3%; Score 57; DB 12; Length 65;
Best Local Similarity 92.3%; Pred. No. 2.9e-06;
Matches 60; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1226 GCTTCCGAGCCCGAGTGTTCGACACATGCGATGAGCATCACTTAGCAACTCAAG 1285
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 GCTTCCGAGCCCGAGTGTTCGATGCATGCATGAGCATCACTTAGCAACTCAAG 60

QY 1286 AACA 1290
    | | | | |
Db 61 AACA 65

RESULT 11
US-10-311-455-1669/c
; Sequence 1669, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Det
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1669
LENGTH: 6668
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
NAME/KEY: unsure
LOCATION: 4733
OTHER INFORMATION: n is a or g or c or t
US-10-311-455-1669

Query Match 4.2%; Score 55.8; DB 12; Length 6668;
Best Local Similarity 57.0%; Pred. No. 9.6e-05;
Matches 102; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 1140 ATATTAAATGATTAACCATTTAAACAAACAGCAAAACAAACAAACAAACAAAC 1199
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 5716 AAAAAAATTAATAAAAAAAAAAAAAAAAAAAAAACAAAAAACAACAAAAA 5657
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 25, 2003, 11:55:10 : Search time 27 Seconds
(without alignments)
1137.605 Million cell updates/sec

Title: US-09-809-545a-2
Perfect score: 1086
Sequence: 1 MTNKKAVNPYTNMGWKLNPVY.....VLSSLDASTYGGYNRFAPY 203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 566894 seqs, 151307093 residues
Total number of hits satisfying chosen parameters: 566894

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep:*
 - 3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
 - 4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep:*
 - 5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
 - 6: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep:*
 - 7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
 - 8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep:*
 - 9: /cgn2_6/ptodata/1/pubppa/US09A_PUBCOMB.pep:*
 - 10: /cgn2_6/ptodata/1/pubppa/US09B_PUBCOMB.pep:*
 - 11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep:*
 - 12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep:*
 - 13: /cgn2_6/ptodata/1/pubppa/US10A_PUBCOMB.pep:*
 - 14: /cgn2_6/ptodata/1/pubppa/US10B_PUBCOMB.pep:*
 - 15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep:*
 - 16: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
 - 17: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
 - 18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------------------|---------------------|
| 1 | 1086 | 100.0 | 203 | 10 US-09-809-545a-2 | Sequence 2, Appl1 |
| 2 | 551 | 50.7 | 330 | 9 US-09-794-591-2 | Sequence 2, Appl1 |
| 3 | 288 | 26.5 | 366 | 12 US-10-359-385-2 | Sequence 2, Appl1 |
| 4 | 116 | 10.7 | 3063 | 12 US-10-301-822-26 | Sequence 26, Appl1 |
| 5 | 116 | 10.7 | 3063 | 12 US-10-177-293-61 | Sequence 61, Appl1 |
| 6 | 116 | 10.7 | 3063 | 12 US-10-177-293-63 | Sequence 63, Appl1 |
| 7 | 96 | 8.8 | 388 | 12 US-10-012-952a-172 | Sequence 172, Appl1 |
| 8 | 96 | 8.8 | 760 | 8 US-08-754-311b-2 | Sequence 2, Appl1 |
| 9 | 93 | 8.6 | 692 | 15 US-10-156-761-14649 | Sequence 14649, A |
| 10 | 92.5 | 8.5 | 919 | 15 US-10-128-714-8387 | Sequence 8387, Ap |
| 11 | 90.5 | 8.3 | 481 | 15 US-10-156-761-112012 | Sequence 112012, A |
| 12 | 89.5 | 8.2 | 342 | 15 US-10-156-761-11221 | Sequence 11221, A |
| 13 | 88.5 | 8.1 | 363 | 15 US-10-156-761-10205 | Sequence 10205, A |
| 14 | 88 | 8.1 | 380 | 15 US-10-156-761-11952 | Sequence 11952, A |
| 15 | 88 | 8.1 | 2116 | 12 US-10-224-999a-3475 | Sequence 3475, Ap |

| | | | | | |
|----|------|-----|-----|------------------------|-------------------|
| 16 | 87.5 | 8.1 | 620 | 15 US-10-156-761-7979 | Sequence 7979, Ap |
| 17 | 87 | 8.0 | 465 | 15 US-10-205-823-136 | Sequence 136, App |
| 18 | 86.5 | 8.0 | 262 | 10 US-09-263-689-14 | Sequence 14, Appl |
| 19 | 86.5 | 8.0 | 262 | 15 US-10-235-674-14 | Sequence 14, Appl |
| 20 | 86.5 | 8.0 | 262 | 15 US-10-235-674-14 | Sequence 14, Appl |
| 21 | 86 | 7.9 | 245 | 9 US-09-796-858-20 | Sequence 20, Appl |
| 22 | 86 | 7.9 | 275 | 12 US-10-313-853-3 | Sequence 3, Appl1 |
| 23 | 86 | 7.9 | 275 | 12 US-09-813-408-21 | Sequence 21, Appl |
| 24 | 86 | 7.9 | 337 | 15 US-10-156-761-12003 | Sequence 12003, A |
| 25 | 86 | 7.9 | 550 | 15 US-10-156-761-11905 | Sequence 11905, A |
| 26 | 86 | 7.8 | 275 | 8 US-08-322-678-7 | Sequence 7, Appl1 |
| 27 | 85 | 7.8 | 275 | 9 US-09-060-854B-3 | Sequence 3, Appl1 |
| 28 | 85 | 7.8 | 275 | 10 US-09-976-414-7 | Sequence 7, Appl1 |
| 29 | 85 | 7.8 | 275 | 10 US-10-324-152-1 | Sequence 1, Appl1 |
| 30 | 85 | 7.8 | 275 | 12 US-09-824-607-1 | Sequence 1, Appl1 |
| 31 | 85 | 7.8 | 275 | 12 US-10-242-549-4 | Sequence 4, Appl1 |
| 32 | 85 | 7.8 | 275 | 14 US-10-075-907-2 | Sequence 2, Appl1 |
| 33 | 85 | 7.8 | 275 | 14 US-10-075-895-2 | Sequence 2, Appl1 |
| 34 | 85 | 7.8 | 275 | 15 US-10-033-325-3 | Sequence 3, Appl1 |
| 35 | 85 | 7.8 | 275 | 15 US-10-228-572-3 | Sequence 3, Appl1 |
| 36 | 85 | 7.8 | 308 | 15 US-10-156-761-13336 | Sequence 13336, A |
| 37 | 85 | 7.8 | 382 | 14 US-10-090-624-31 | Sequence 31, Appl |
| 38 | 85 | 7.8 | 382 | 15 US-10-033-325-2 | Sequence 2, Appl1 |
| 39 | 85 | 7.8 | 382 | 15 US-10-104-693-2 | Sequence 2, Appl1 |
| 40 | 85 | 7.8 | 382 | 15 US-10-228-572-2 | Sequence 2, Appl1 |
| 41 | 84.5 | 7.8 | 623 | 15 US-10-156-761-11120 | Sequence 11120, A |
| 42 | 84 | 7.7 | 146 | 15 US-10-156-761-8967 | Sequence 8967, Ap |
| 43 | 84 | 7.7 | 275 | 11 US-09-813-408-18 | Sequence 18, Appl |
| 44 | 83.5 | 7.7 | 485 | 10 US-09-925-300-1664 | Sequence 1664, Ap |
| 45 | 83.5 | 7.7 | 584 | 15 US-10-156-761-12405 | Sequence 12405, A |

ALIGNMENTS

RESULT 1
US-09-809-545a-2
; Sequence 2, Application US/09809545A
; Patent No. US2002010804A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, Lawrence W.
; APPLICANT: White, R. Tyler
; TITLE OF INVENTION: SECRETED FACTORS
; FILE REFERENCE: SCIOS.017A
; CURRENT APPLICATION NUMBER: US/09/809,545A
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-09-809-545a-2

| | | | | |
|-----------------------|----------------|---|----------|------------|
| Query Match | 100.0% | Score 1086 | DB 10 | Length 203 |
| Best Local Similarity | 100.0% | Pred. No. 9 | 7e-99 | |
| Matches 203 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |
| QY | 1 | MTNKKAVNPYTNMGWKLNPVYGAVYSPDFAGTYLLCOANDESSMTSGPSSLYTSAMG | 60 | |
| DB | 1 | MTNKKAVNPYTNMGWKLNPVYGAVYSPDFAGTYLLCOANDESSMTSGPSSLYTSAMG | 60 | |
| QY | 61 | FPYPATTAATAAAYGALHGRGRTVYTFPRAAPPPPIPAVGGVYOEPYGNKLLGGYA | 120 | |
| DB | 61 | FPYPATTAATAAAYGALHGRGRTVYTFPRAAPPPPIPAVGGVYOEPYGNKLLGGYA | 120 | |
| QY | 121 | AYRYAOPPTATAAAYSDSYGRVYAADPYHHTLAPATYGVGAMNAFPLTDKTRSHAD | 180 | |
| DB | 121 | AYRYAOPPTATAAAYSDSYGRVYAADPYHHTLAPATYGVGAMNAFPLTDKTRSHAD | 180 | |
| QY | 181 | VGLVLSLDASTYGGYNRFAPY 203 | | |
| DB | 181 | VGLVLSLDASTYGGYNRFAPY 203 | | |

RESULT 2
US-09-794-591-2
; Sequence 2, Application US/09794591
; Patent No. US20010018198A1
; GENERAL INFORMATION:
; APPLICANT: Pulst, Stefan M.
; APPLICANT: Shidota, Hiroki
; TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
; FILE REFERENCE: CE 3093
; CURRENT APPLICATION NUMBER: US/09/794,591
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/145,391
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-591-2

Query Match 50.7%; Score 551; DB 9; Length 330;
Best Local Similarity 97.1%; Pred. No. 5,5e-46;
Matches 102; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MTNKAANPYTNGMKLNPNVGAIVSPDFYAGTVLLCOANOGSSMYSGPSSLVYTSAMPG 60
DB 136 MTNKAANPYTNGMKLNPNVGAIVSPDFYAGTVLLCOANOGSSMYSGPSSLVYTSAMPG 255
QY 61 FPPYATAAAAYRGAHLRGRTVYNTFRAAAPPPPIPAYGCVVY 105
DB 236 FPPYATAAAAYRGAHLRGRTVYNTFRAAAPPPPIPAYGCVVY 300

RESULT 3
US-10-359-385-2
; Sequence 2, Application US/10359385
; Publication No. US20030143622A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guejler, Karl J.
; APPLICANT: Lu, Alina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/10/359,385
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/176,657
; PRIOR FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1250374
US-10-359-385-2

Query Match 26.5%; Score 288; DB 12; Length 366;
Best Local Similarity 48.9%; Pred. No. 4e-20;
Matches 68; Conservative 11; Mismatches 54; Indels 6; Gaps 4;
QY 1 MTNKAANPYTNGMKLNPNVGAIVSPDFYAGTVLLCOANOGSSMYSGPSSLVYTSAMPG 56
DB 190 MTNKAANPYTNGMKLNPNVGAIVSPDFYAGTVLLCOANOGSSMYSGPSSLVYTSAMPG 249
QY 57 AMPGPYR-AAATAAAAYRGAHLRGRTVYNTFRAAAPPPPIPAYGCVVYDEPYGNKLL 115

DB 250 IIPGFPYPTAATTAARAHNRGRRTYGAVR-AVPTALPAYGVDMOPTDMHSLLL 308
QY 116 OCGYAARYAOPTPATAA 134
DB 309 QPQPLLOPLQPLTYVMA 327

RESULT 4
US-10-301-822-26
; Sequence 26, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kametkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; FILE REFERENCE: MPW01-029P2RNM
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MPW01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 3063
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-26

Query Match 10.7%; Score 116; DB 12; Length 3063;
Best Local Similarity 25.1%; Pred. No. 0.043;
Matches 45; Conservative 16; Mismatches 54; Indels 64; Gaps 8;
QY 50 SLYVTSAMPGPYPTAATAAAYR-GAHLRGRTV-----YNTFRAA 92
DB 2078 NNVILOPLQPLTPY-KIVIAVYEDGCHLGNKRTYGLPPONIHISDEYTFRRSW 2136
QY 93 PEPPIPAYGVVYDEPYGNKLLQ--GGYAARYAOPTPATAAAYSDSYGRVYAADPYH 149
DB 2137 DPSPSPVLGYKIVKPVGSNEPMEAFVGEKMTSYTL----- 2171
QY 150 HTLAPAPYGVGAMNAFA-----PLTDAKTRSHADVGVLSSLASTYGGYKRF 200
DB 2172 HNLNPTTYDY--NVYAQYDSGLSVPLTDGTT-----LYLNVTDLKTYQIGMDTF 2220

RESULT 5
US-10-177-293-61
; Sequence 61, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatf, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Ganavarpur, Manjula
; APPLICANT: Kametkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian

```

: APPLICANT: Monahan, John
: APPLICANT: Meyers, Rachel E.
: APPLICANT: Bast Jr., Robert C.
: APPLICANT: Hortobagyi, Gabriel N.
: APPLICANT: Puzsatic, Lajos
: APPLICANT: Meric, Funda
: APPLICANT: Sahlin, Aysegul B.
: APPLICANT: Mills, Gordon B.
: TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
: TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
: FILE REFERENCE: MRI-038
: CURRENT APPLICATION NUMBER: US/10/177,293
: CURRENT FILING DATE: 2002-06-21
: PRIOR APPLICATION NUMBER: US 60/299,887
: PRIOR FILING DATE: 2001-06-21
: PRIOR APPLICATION NUMBER: US 60/301,572
: PRIOR FILING DATE: 2001-06-27
: PRIOR APPLICATION NUMBER: US 60/306,501
: PRIOR FILING DATE: 2001-07-18
: PRIOR APPLICATION NUMBER: US 60/325,002
: PRIOR FILING DATE: 2001-09-25
: PRIOR APPLICATION NUMBER: US 60/362,585
: PRIOR FILING DATE: 2002-03-05
: PRIOR APPLICATION NUMBER: US 60/xxx,xxx
: PRIOR FILING DATE: 2002-05-14
: NUMBER OF SEQ ID NOS: 506
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 61
: LENGTH: 3063
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-177-293-61

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Query Match      10.7%  Score 116; DB 15; Length 3063;
Best Local Similarity 25.1%; Pred. No. 0.043;
Matches 45; Conservative 16; Mismatches 54; Indels 64; Gaps 8;

OY 50 SSVYTSAMPGFPYPAATAAAYR---GAHLRGGRVY-----YNTFRAAA 92
DB 2078 NNVLIOPLQPTPT-KitVIAVYEDGGHLTGNGRTYGLPPONIHISDEMYTRFRVSW 2136
OY 93 PPPIPAYGVVYOEPEVYGNKLLQ---GGVAAARYAOPTPATAAAYSDSYGRVYAADPYH 149
DB 2137 DPSPSPVLYGKIVKPKVGSNPEMEAFVGEKTSYTL----- 2171
OY 150 HTLAPAPYGYGAMNAFA-----PLTDAKTRSHADVGVLVSLQASLYOGGYNRF 200
DB 2172 HNLNPSTTYDV---NVYAQYDSGLSVPLTDGTT-----LYLWVTDLKTYYQIGWDTF 2220

```

RESULT 6
US-10-177-293-63

```

: Sequence 63, Application US/10177293
: Publication No. US20030124128A1
: GENERAL INFORMATION:
: APPLICANT: Lillie, James
: APPLICANT: Glatt, Karen
: APPLICANT: Zhao, Xumel
: APPLICANT: Gannavarpu, Manjula
: APPLICANT: Kamatkar, Shubhangi
: APPLICANT: Mertens, Maureen
: APPLICANT: Myer, Vic
: APPLICANT: Wang, Youzhen
: APPLICANT: Xu, Yongyao
: APPLICANT: Hoersch, Sebastian
: APPLICANT: Monahan, John
: APPLICANT: Meyers, Rachel E.
: APPLICANT: Bast Jr., Robert C.
: APPLICANT: Hortobagyi, Gabriel N.
: APPLICANT: Puzsatic, Lajos
: APPLICANT: Meric, Funda
: APPLICANT: Sahlin, Aysegul
: APPLICANT: Mills, Gordon B.

```

```

: TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT
: TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
: FILE REFERENCE: MRI-038
: CURRENT APPLICATION NUMBER: US/10/177,293
: CURRENT FILING DATE: 2002-06-21
: PRIOR APPLICATION NUMBER: US 60/299,887
: PRIOR FILING DATE: 2001-06-21
: PRIOR APPLICATION NUMBER: US 60/301,572
: PRIOR FILING DATE: 2001-06-27
: PRIOR APPLICATION NUMBER: US 60/306,501
: PRIOR FILING DATE: 2001-07-18
: PRIOR APPLICATION NUMBER: US 60/325,002
: PRIOR FILING DATE: 2001-09-25
: PRIOR APPLICATION NUMBER: US 60/362,585
: PRIOR FILING DATE: 2002-03-05
: PRIOR APPLICATION NUMBER: US 60/xxx,xxx
: PRIOR FILING DATE: 2002-05-14
: NUMBER OF SEQ ID NOS: 506
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 63
: LENGTH: 3063
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-177-293-63

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Query Match      10.7%  Score 116; DB 15; Length 3063;
Best Local Similarity 25.1%; Pred. No. 0.043;
Matches 45; Conservative 16; Mismatches 54; Indels 64; Gaps 8;

OY 50 SSVYTSAMPGFPYPAATAAAYR---GAHLRGGRVY-----YNTFRAAA 92
DB 2078 NNVLIOPLQPTPT-KitVIAVYEDGGHLTGNGRTYGLPPONIHISDEMYTRFRVSW 2136
OY 93 PPPIPAYGVVYOEPEVYGNKLLQ---GGVAAARYAOPTPATAAAYSDSYGRVYAADPYH 149
DB 2137 DPSPSPVLYGKIVKPKVGSNPEMEAFVGEKTSYTL----- 2171
OY 150 HTLAPAPYGYGAMNAFA-----PLTDAKTRSHADVGVLVSLQASLYOGGYNRF 200
DB 2172 HNLNPSTTYDV---NVYAQYDSGLSVPLTDGTT-----LYLWVTDLKTYYQIGWDTF 2220

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RESULT 7
US-10-012-952A-172

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: Sequence 172, Application US/10012952A
: Publication No. US20030175707A1
: GENERAL INFORMATION:
: APPLICANT: Sun, Yongming
: APPLICANT: Recipon, Herve
: APPLICANT: Chen, Sei-Yu
: TITLE OF INVENTION: Composition and Methods Relating to Prostate Specific Genes an
: FILE REFERENCE: DEX-0263
: CURRENT APPLICATION NUMBER: US/10/012,952A
: CURRENT FILING DATE: 2001-11-06
: PRIOR APPLICATION NUMBER: US 60/246,039
: PRIOR FILING DATE: 2000-11-06
: NUMBER OF SEQ ID NOS: 248
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 172
: LENGTH: 388
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-012-952A-172

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Query Match      8.8%  Score 96; DB 12; Length 388;
Best Local Similarity 24.9%; Pred. No. 0.3;
Matches 59; Conservative 16; Mismatches 86; Indels 76; Gaps 11;

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OY 21 GAVYSPDYACTVLLCONQSGSSMYSGPSSL-----VYTSAMGFFYPAATAAAYRG 74
DB 67 GGNFSVAAAAMAAAAAANQ--CRNLMAHPAPLAPGASAYSSA--PGEAPPSAAAAAAA 124
OY 75 AHLRGRTVYNTFRFAAPPPPIPAYGVVYQ-----EPVYGNKLLQGYAAYRY-- 124

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8387
; LENGTH: 919
; TYPE: PRF
; ORGANISM: Aspergillus fumigatus
US-10-128-714-8387

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```

Query Match      8.5%; Score 92.5; DB 15; Length 919;
Best Local Similarity 28.6%; Pred. No. 1.9;
Matches 36; Conservative 10; Mismatches 61; Indels 19; Gaps 5;

```

```

QY 57 AMGFYPAATAAAVGAHLRGRVTYNTFRAAAPPEIPAVGVYQEPYGNKLLQ 116
DB 47 AYAGFAFEIGSGANALGGLPAGGS--YGA-----PPQPAAG--YQAPYGAADPSQ 96
QY 117 GGYAARYAAPTATATAASDSYGRYAADPHHTLAPATYGVGAMNAPL----- 169
DB 97 MNAAAGYAPATPPTGIAQMTQDFGAMGVDP--HLMPPQPAVAVPAAPRPVPLNQLYP 154
QY 170 TDAKTR 175
DB 155 TDLTLQ 160

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```

RESULT 11
US-10-156-761-12012
; Sequence 12012, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: SHIBATA, YOSHIOKI
; APPLICANT: SAKAKI, YOSHIOKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 12012
; LENGTH: 481
; TYPE: PRF
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12012

```

```

Query Match      8.3%; Score 90.5; DB 15; Length 481;
Best Local Similarity 28.0%; Pred. No. 1.3;
Matches 47; Conservative 11; Mismatches 75; Indels 35; Gaps 7;

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```

QY 26 PDFYAGTVLLCQANOGSSMYSGPSS---LYVTS-AMGFYPAATAAAVGAHLRGR 80
DB 298 PDSSSAVLIREFGAGAGAGAGASEGRKTCLSOSSSECVETAPPCGAMGASVAAADLDCD 357
QY 81 GRTVNTFRAAAPPEIPAVG-----GVYQEPYGNKLLGQYARYAAPTAT 131
DB 358 G-----AELVVGAPGEGVSLKSGSVTVLDGSEGPLSGSVT---YTQMTPTGI 404
QY 132 --AAAYSDSYGRYAADPHHTLAPATYGVGAMNAPL-----FAPLTD 171
DB 405 PGTAETADRFAGATLTAGPYHPGGRPLATGAPGENAKGCVWVPTTD 452

```

```

RESULT 12
US-10-156-761-11221
; Sequence 11221, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:

```

```

; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBATA, YOSHIOKI
; APPLICANT: SAKAKI, YOSHIOKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 11221
; LENGTH: 342
; TYPE: PRF
; ORGANISM: Streptomyces avermitilis
US-10-156-761-11221

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Query Match      8.2%; Score 89.5; DB 15; Length 342;
Best Local Similarity 24.6%; Pred. No. 1.1;
Matches 52; Conservative 22; Mismatches 88; Indels 49; Gaps 11;

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QY 6 AVNPYNGKLNLYV---GAVYSPDYAGTVLLCQANOGSSMYSGPSSLYTSAMPGP 62
DB 56 ALDPRLVORVEAVETLGSAYGLDSAGYMANLEQRORVRRGPPPAHVY----- 106
QY 63 YPATAAAV---RGALRGR-----GRVYNTFRAAAPPEIP-----AV 100
DB 107 -PYVPAACVFDLGRGDFRPRPAATGKRAVEAAASEPAPVPEGCVAGTGAVYGQK 165
QY 101 GGYVQEPYGNKLLGQYARYAAPT--PATAAAYSQY-GR-VYAADPHHTLAPAP 156
DB 166 GGVTASTVYSGSITVAALVANAAGSTVDPETGVLYGELFGQGVVYPADGVHEA-ARRR 224
QY 157 TYVGAMNAPL-----TDK-TRSHA 178
DB 225 LAETAANKNAPPPLNTTLAVVATDAELTKAQA 255

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RESULT 13
US-10-156-761-10205
; Sequence 10205, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBATA, YOSHIOKI
; APPLICANT: SAKAKI, YOSHIOKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10205
; LENGTH: 363
; TYPE: PRF
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10205

```

```

Query Match      8.1%; Score 88.5; DB 15; Length 363;
Best Local Similarity 26.9%; Pred. No. 1.5;
Matches 50; Conservative 14; Mismatches 51; Indels 71; Gaps 12;

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OY 65 AATAAAYRGAN-LRGR-----GRTVYNTFRA-----AAPP- 94
DB 191 AKTLEAVGRGROKHLGRISADDLGALTDDGTPVQHTSDADYLAGLADIGNTPDQGSAPPQ 250
OY 95 ----PRPAAVGVYQEPVYGNKLLGGYAAVRYAQPP-----ATAAAYSDSYGVYAA 145
DB 251 TPQAPETPA-----QPOY-----GGQDAVAYQOQTPDPYGYQOQYGGQDAYGYOPTA 297
OY 146 DPVHHTLAPAPTYGVGANNAF-----APLT-DAKTRSH-ADDVGL----VLSSLOA 190
DB 298 DPY-----AAYPQOQIGDOGTATDQNNQOQYSGPQTHTDSQPAQHDDEASLFTSMISAOQL 353
OY 191 SIYOGG 196
DB 354 RAYEOG 359
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RESULT 14

S-10-156-761-11952

Sequence 11952, Application US/10156761

Publication No. US20030119018A1

GENERAL INFORMATION:

```
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11952
LENGTH: 380
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-11952
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Query Match

8.1%; Score 88; DB 15; Length 380;

Best Local Similarity 25.1%; Pred. No. 1.8;

Matches 53; Conservative 15; Mismatches 61; Indels 82; Gaps 11;

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49 PSSLVYTSAMPGFPY-----PATA-----AAAYRGANLR-----GGRITY 85
DB 96 PSTVAYT-----GFPWHMIREELRLRPQTTLFVDLHADAEWHLRTGPDAGRAALY 151
OY 86 NTFRAAAPPP-----IPAY-----GGVYOR-----P 108
DB 152 G---RVAPPPRRRYAPPAIYKAVATILRSCHRPPEYVLEHQAALGRVAHEGSHADIVLTP 208
OY 109 VYGNKLLGGYA---AYRYAQTPTATAAAYSDSYGVYAADPYHHTLAPAPTYG---VG 161
DB 209 FCGGAALPGFVPGPAPYPPEDPRPRTPDG-----PAAADVHNTIAAAVRAGRHGEAD 260
OY 162 AMNAFAPLTDAKTRSHADVGLVLSLOAST 192
DB 261 ALAAQMEQTAASTHGAASEALHMRREVRA DL 291
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RESULT 15

US-10-224-999A-3475

Sequence 3475, Application US/10224999A

Publication No. US20030171318A1

GENERAL INFORMATION:

```
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
```

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APPLICANT: Zavitz, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Composition and Method for Treating Viral Infection
FILE REFERENCE: 5004.01
CURRENT APPLICATION NUMBER: US/10/224,999A
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/313,695
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 3484
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3475
LENGTH: 2116
TYPE: PRT
ORGANISM: Rubella virus
US-10-224-999A-3475
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Query Match

8.1%; Score 88; DB 12; Length 2116;

Best Local Similarity 31.7%; Pred. No. 15;

Matches 39; Conservative 8; Mismatches 50; Indels 26; Gaps 7;

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OY 43 SSMYSGPSSLVYTSAMPGFPYPAATAAAYRGANLRGRTVYNTFRAAPP---PRIPA 99
DB 708 AAVRAGPQGSATSPPGDPPPRARRSQR--HLDAGTTPPAPARPPPPAPSPAPAP 765
OY 100 YGVVYQEPVYGNKLLGGYAAVRYAQ-----PTPATAAAYSD---SYGVYAAD 146
DB 766 RAG---DPVLPTS--AGPADRARHAELEVAEYSPSPPTPKADPDSDIVESYAR--AAG 817
OY 147 PYH 149
DB 818 PVH 820
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Search completed: September 25, 2003, 12:07:56

Job time : 28 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 25, 2003, 11:56:35 ; Search time 53 Seconds
(without alignments)
1690.581 Million cell updates/sec

Title: US-09-809-545A-2
Perfect score: 1086
Sequence: 1 MTNKKAVNPYTNKMLNPVY.....VLSSQASIXQGYNRPAPY 203

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL-frame+ p2n.model -DEV-x1p
-Q/cgn2_1/USFTO.spool_P/US0980955/runat_25092003.111104.22915/app_query.fasta.1.391
-DB-issued.patents_NA -QFMT=fastap -SUFFIX=ini -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bls0sum62 -TRANS=human40.cdi
-LIST=45 -DOCCALIGN=200 -THR.SCORE=pcr -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRR=US09809545 @CGN.1.1.85 @runat_25092003.111104.22915 -NCPu=6 -ICPu=3
-NO_MMAP -LAREQUERY -NEG_SCORES=0 -WAIT -DSBBLOCK=100 -LOGNGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCBUS.COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|---------|-------|-------------------|
| 1 | 955 | 87.9 | 2372 | 3 | US-09-145-391-1 |
| 2 | 467.5 | 43.0 | 1506 | 3 | US-09-176-657-5 |
| 3 | 467.5 | 43.0 | 1506 | 4 | US-09-421-399-5 |
| 4 | 101 | 9.3 | 914 | 2 | US-08-935-450-10 |
| 5 | 98.5 | 9.1 | 821 | 3 | US-08-990-823-62 |
| 6 | 98.5 | 9.1 | 821 | 3 | US-09-477-135A-62 |
| 7 | 97.5 | 9.0 | 4403765 | 3 | US-09-103-840A-2 |
| 8 | 97.5 | 9.0 | 4411529 | 3 | US-09-103-840A-1 |
| 9 | 96 | 8.8 | 3231 | 1 | US-08-195-152-1 |
| 10 | 94.5 | 8.7 | 4403765 | 3 | US-09-103-840A-2 |
| 11 | 94 | 8.7 | 2368 | 4 | US-09-343-011B-3 |
| 12 | 94 | 8.7 | 43280 | 2 | US-08-804-227C-1 |

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|----|------|-----|---------|---|----------------------|--------------------|
| 13 | 92.5 | 8.5 | 2371 | 2 | US-08-343-443B-1 | Sequence 1, Appl1 |
| 14 | 92.5 | 8.5 | 2412 | 1 | US-08-437-027-18 | Sequence 1b, Appl |
| 15 | 92.5 | 8.5 | 28958 | 1 | US-08-258-261B-6 | Sequence 6, Appl1 |
| 16 | 92.5 | 8.5 | 28958 | 1 | US-08-456-837-6 | Sequence 6, Appl1 |
| 17 | 92.5 | 8.5 | 28958 | 1 | US-08-457-342-6 | Sequence 6, Appl1 |
| 18 | 92.5 | 8.5 | 28958 | 1 | US-08-457-646A-6 | Sequence 6, Appl1 |
| 19 | 92.5 | 8.5 | 28958 | 1 | US-08-458-076A-6 | Sequence 6, Appl1 |
| 20 | 92.5 | 8.5 | 28958 | 1 | US-08-764-233A-4 | Sequence 4, Appl1 |
| 21 | 92.5 | 8.5 | 28958 | 1 | US-08-457-135A-6 | Sequence 6, Appl1 |
| 22 | 92.5 | 8.5 | 28958 | 1 | US-08-729-214-6 | Sequence 6, Appl1 |
| 23 | 92.5 | 8.5 | 28958 | 3 | US-09-028-934-6 | Sequence 6, Appl1 |
| 24 | 92.5 | 8.5 | 49377 | 1 | US-08-764-233A-1 | Sequence 1, Appl1 |
| 25 | 92.5 | 8.5 | 53526 | 3 | US-08-658-136-2 | Sequence 2, Appl1 |
| 26 | 92 | 8.5 | 53577 | 3 | US-08-658-136-1 | Sequence 1, Appl1 |
| 27 | 91 | 8.4 | 1896 | 4 | US-09-343-011B-4 | Sequence 4, Appl1 |
| 28 | 90.5 | 8.3 | 852 | 4 | US-08-252-991A-16108 | Sequence 16108, A |
| 29 | 90.5 | 8.3 | 1311 | 4 | US-08-252-991A-16493 | Sequence 16493, A |
| 30 | 90.5 | 8.3 | 10095 | 3 | US-08-822-586-45 | Sequence 45, Appl |
| 31 | 90 | 8.3 | 2303 | 4 | US-09-932-146-3 | Sequence 3, Appl1 |
| 32 | 89.5 | 8.2 | 4411529 | 3 | US-09-103-840A-1 | Sequence 1, Appl1 |
| 33 | 89 | 8.2 | 1083 | 4 | US-09-252-991A-8817 | Sequence 8817, Ap |
| 34 | 89 | 8.2 | 1140 | 3 | US-09-023-173-4 | Sequence 4, Appl1 |
| 35 | 89 | 8.2 | 1227 | 4 | US-09-252-991A-9232 | Sequence 9232, Ap |
| 36 | 89 | 8.2 | 1296 | 4 | US-09-252-991A-9150 | Sequence 9150, Ap |
| 37 | 89 | 8.2 | 2715 | 4 | US-09-252-991A-8715 | Sequence 8715, Ap |
| 38 | 88.5 | 8.1 | 2007 | 4 | US-09-252-991A-3308 | Sequence 3308, Ap |
| 39 | 88.5 | 8.1 | 2709 | 4 | US-09-252-991A-3326 | Sequence 3326, Ap |
| 40 | 88 | 8.1 | 885 | 4 | US-08-252-991A-4426 | Sequence 4426, Ap |
| 41 | 88 | 8.1 | 1362 | 4 | US-09-442-100-7 | Sequence 4184, Ap |
| 42 | 88 | 8.1 | 2923 | 6 | US-09-252-991A-4184 | Patent No. 5187076 |
| 43 | 87.5 | 8.1 | 3155 | 4 | US-09-442-100-7 | Sequence 7, Appl1 |
| 44 | 87.5 | 8.1 | 3155 | 4 | US-08-939-106-7 | Sequence 7, Appl1 |
| 45 | 87.5 | 8.1 | 44377 | 2 | US-08-804-227C-7 | Sequence 7, Appl1 |

ALIGNMENTS

RESULT 1
US-09-145-391-1
Sequence 1, Application US/09145391
Patent No. 6194171
GENERAL INFORMATION:
APPLICANT: Pulist, Stefan M.
APPLICANT: Shibata, Hiroki
TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins.
TITLE OF INVENTION: Products Related Thereto and Methods of Using Same
FILE REFERENCE: CE 3093
CURRENT APPLICATION NUMBER: US/09/145.391
CURRENT FILING DATE: 1998-09-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2372
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (987)..(1979)
US-09-145-391-1

Alignment Scores:

Pred. No.: 2.56e-85
Score: 955.00
Percent Similarity: 86.94%
Best Local Similarity: 85.14%
Query Match: 87.94%
DB: 3
Caps: 2
US-09-809-545A-2 (1-203) x US-09-145-391-1 (1-2372)

QY 1 MetThrAsnLysLysAlaValAsnProTyrThrAsnGlyTrpLysLeuAsnProValVal 20
Db 1572 ATGACAAATATAAAGACCGTCACCCCTTATACAAATGCTGGAATTTGATTCACGTTGTC 1631

```

QY 21 GYALAVATYrSerProAspPheTYrAlaGlyThrValLeuLeuGlnAlaAsnGln 40
DB 1632 GGTGAGCTACAGTCCGCAATTCATGACGACGAGCTCTGTGGCCAGCCAAACGAG 1691
QY 41 GUGlySerSerMetTySerGlyProSerSerLeuValTYrThrSerAlaMetProGly 60
DB 1692 GAGGAGATCTTCATGACGATGACGACCCCTTCACTGTATATACCTTCCAAATGCCAGGC 1751
QY 61 PheProTYrProAlaAlaThrAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 80
DB 1752 TTCGCGATCCAGACACCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1811
QY 81 GYATgThValTYrAsnThrPheArgAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 100
DB 1812 GGTGCGACCGGTACAAACCTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1871
QY 101 GYGLYValValTYr-GInGluProValTYrGlyValLeuLeuGlnGlyTYrAl 120
DB 1872 GCGGCTGTGTGTACCCAGAGATGATTTATGTGCGAGAC--ATTATATGCTGTTATGC 1928
QY 120 AlaTYrArgTYrAlaGlnProThrProAlaThrAlaAlaAlaAlaAlaAlaAlaAlaAla 138
DB 1929 TGCATACCCCTACGCCACACCTTACCCCTGCGCTGCGCTACAGTACAG--AAATC 1987
QY 139 -----TYrGlyArgVal 142
DB 1988 AGTTCGCTTCCTGCGACGAGATGAATTTCTGTAAACCTCTGCGAGTTACGAGACGAGT 2047
QY 142 LTYrAlaAlaAspProTYrHisHisThrLeuAlaProAlaProAlaProAlaProAlaPro 162
DB 2048 TTATGCTGCCGACCCCTTACACGACGACCTGCTGCGACCCGCGCGCGCGCGCGCGCG 2107
QY 162 ametaAlaPheAlaProLeuThrAspAlaLysThrArgSerHisAlaAspValAl 182
DB 2108 CATGATGCTTTTGACCTTTCACATGATGCCAAAGCTAGAGCCATGCTGATGATGTGG 2167
QY 182 yLeuValLeuSerSerLeuGlnAlaSerIleTYrGlnGlyTYrAsnArgPheAlaPro 202
DB 2168 TCTGCTTCTTCTTCATGTCAGGCTAGTATATACGAGGGGATACACACGTTTTCCTCC 2227
QY 202 OTTYr 203
DB 2228 ATAC 2231

```

RESULT 2 US-09-176-657-5

Sequence 5, Application US/09176657
Patent No. 6020164

GENERAL INFORMATION:

APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Lu, Alina
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
FILE REFERENCE: PF-0611 US
CURRENT APPLICATION NUMBER: US/09/176, 657
CURRENT FILING DATE: 1998-10-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PERL Program
SEQ ID NO 5
LENGTH: 1506
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: -
OTHER INFORMATION: 1250374
US-09-176-657-5

Alignment Scores: 2,846-37 Length: 1506
Pred. No.: 467.50 Matches: 107
Score:

Percent Similarity: 56.48% Conservative: 15
Best Local Similarity: 49.54% Mismatches: 39
Query Match: 43.05% Indels: 56
DB: 3 Gaps: 8

US-09-809-545a-2 (1-203) x US-09-176-657-5 (1-1506)

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QY 1 MetThrAsnLysLysAlaValAsnProTYrThrAsnGlyTYrLysLeuAsnProValVal 20
DB 768 ATGACCAATTAAGAGATGTTACACCATATGCAAAATGCTTGAATTAAGCCAGATGT 827
QY 21 GYALAVATYrSerProAspPheTYrAlaGlyThrValLeuLeuGlnAlaAsn--- 39
DB 828 GGAGCTGTATATGTCGCGAGATATATGACGATTCAGGCTTCAAGACAGATGTGCCCTTA 887
QY 40 ---GInGlySerSerMetTySerGlyProSerSerLeuValTYrThrSer 56
DB 888 GGCATATGATGACAGAGTCCCTATCAGGAGAGAGGGGATATACACTTACATTCCCTTTA 947
QY 57 AlaMetProGlyPheProTYrPro---AlaAlaThrAlaAlaAlaAlaAlaAlaAlaAla 75
DB 948 ATCATTCCTGCTTCCCTTACCTTACCTGACGACGACGACGACGCGCTTTCAGAGAGCC 1007
QY 76 HisLeuArgGlyArgGlyArgThrValTYrAsnThrPheArgAlaAlaAlaProPro 95
DB 1008 CATTTGAGGGGACAGAGGGGACAGATATATGTGTCAGTCCGA---GCGGTACTCTCCACA 1064
QY 96 ProIleProAlaTYrGlyValValTYrGlnGluProValTYrGlyValLeuLeu 115
DB 1065 GCCATCCCGCGCTATCC----- 1081
QY 116 GInGlyGlyTYrAlaAlaAlaTYrArgTYrAlaGlnProThrProAlaThr----- 131
DB 1082 AGGGGTGATATGACGACCTTACAGATATGACAGCCTGTACTACCTCAACCCGACCCGCT 1141
QY 132 -----AlaAlaAlaTYrSerAspSerTYrGlyArgValTYrAlaAlaAspPro 147
DB 1142 GCTGACGCGCTGACGCGCTTACAGTGCAGTGTATAGGAGGGTATACACACCGACCCGCT 1201
QY 148 TYrHisHisThrLeuAlaProAlaProAlaProTYrGlyValGlyAlaMetAsnAlaPheAla 167
DB 1202 TAC---CATGCCCTTCCCTCCCTGCGCTACTGAGAGTGGCGCTGTG----- 1246
QY 168 ProLeuThrAspAlaLysThrArgSerHisAlaAspValGlyLeuValLeuSerSer 187
DB 1246 ----- 1246
QY 188 LeuGlnAlaSerIleTYrGlnGlyTYrAsnArgPheAlaProTYr 203
DB 1247 -----GCGAGTTTATACCGAGGTGGCTACACCGCATTTGCCCTTAC 1288

```

RESULT 3

US-09-421-299-5
Sequence 5, Application US/09421299

GENERAL INFORMATION:

APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Lu, Alina
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
FILE REFERENCE: PF-0611 US
CURRENT APPLICATION NUMBER: US/09/421, 299
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: 09/176, 657
EARLIER FILING DATE: 1998-10-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PERL Program
SEQ ID NO 5
LENGTH: 1506
TYPE: DNA

ORGANISM: Homo sapiens
FEATURE: -
OTHER INFORMATION: 1250374
US-09-421-299-5

Alignment Scores:

| Pred. No.: | 2,84e-37 | Length: | 1506 |
|------------------------|----------|---------------|------|
| Score: | 467.50 | Matches: | 107 |
| Percent Similarity: | 56.48% | Conservative: | 15 |
| Best Local Similarity: | 49.54% | Mismatches: | 39 |
| Query Match: | 43.05% | Indels: | 56 |
| DB: | 4 | Gaps: | 8 |

US-09-809-545a-2 (1-203) x US-09-421-299-5 (1-1506)

```
QY      1 MethrAsnLysLysAlaValAsnProTyrThrAsnGlyTyrLysLeuAsnProVal 20
      |||
      768 ATGACCAATGAGAGATGTCACACCATATGCAAAATGTTGAATTAACCCAGAGATT 827
QY      21 GAlaValTyrSerProAspPheTyrAlaGlyThrValLeuLeuGlyAlaAsn 39
      |||
      828 GAGAGCTATATGCTCGGAGATTATATGACGATCCAGCTTTCAGCAGATGTCTCTTA 887
QY      40 ---GlnGlySerSerMetTyrSerGlyProSerSerLeu-----ValTyrThrSer 56
      |||
      888 GGCATATGATGCACAGTGCCTATATGAGAAAGGGGATCAACATTCATTCCTTTA 947
QY      57 AlameProGlyPheProTyrPro---AlaAlaThrAlaAlaAlaTyrAlaGlyAla 75
      |||
      948 ATCATTCCTGCTCCCTTACCTACTGTCAGCACACCGGACCCGCTTTCAGAGAGGCC 1007
QY      76 HisLeuArgLysArgGlyArgThrValTyrAsnThrPheArgAlaAlaAlaProPro 95
      |||
      1008 CATTTGAGGGGAGAGGGCGGACAGTATATGTCAGTCCGA---GGGTACTCCACACA 1064
QY      96 ProIleProAlaTyrGlyGlyValValTyrGlnGluProValTyrGlyAsnLysLeu 115
      |||
      1065 GCCATCCCCCGCTATCC-----
      1081
QY      116 GlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaPhe 131
      |||
      1082 AGGGGTGATATGACGCTACAGATATGACAGGCTGCTACTGACACCGGACCGACCGCT 1141
QY      132 -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspPro 147
      |||
      1142 GCTGACAGCCGCTGACGCGCTTACAGTACGAGGTTATGCGAGGCTGTCACAGCGACCC 1201
QY      148 TyrHisHisThrLeuAlaProAlaProThrTyrGlyValGlyAlaMetAsnAlaPheAla 167
      |||
      1202 TAC---CATGCCCTTGGCCCTGCCGCTAGCTATGAGATGGCGCTGTG----- 1246
QY      168 ProLeuThrAspAlaLysThrArgSerHisAlaAspAspValGlyLeuValLeuSerSer 187
      |||
      1246 -----
      1246
QY      188 LeuGlnAlaSerIleTyrGlnGlyGlyTyrAsnArgPheAlaProTyr 203
      |||
      1247 -----GCGAGTTTATACGACAGGTGCTACAGCGGATTTGCCCTTAC 1288
```

RESULT 4
US-08-935-450-10
Sequence 10, Application US/08935450
Patent No. 5977311
GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Yang, Meljia
APPLICANT: Schulz, Vincent
TITLE OF INVENTION: 53BP2 COMPLEXES
FILE REFERENCE: 7934-054
CURRENT APPLICATION NUMBER: US/08/935,450
CURRENT FILING DATE: 1997-09-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentl Ver. 2.0

SEQ ID NO 10
LENGTH: 914
TYPE: DNA
ORGANISM: Homo sapiens
US-08-935-450-10

Alignment Scores:

| Pred. No.: | 0.303 | Length: | 914 |
|------------------------|--------|---------------|-----|
| Score: | 101.00 | Matches: | 48 |
| Percent Similarity: | 37.06% | Conservative: | 15 |
| Best Local Similarity: | 28.24% | Mismatches: | 59 |
| Query Match: | 9.30% | Indels: | 48 |
| DB: | 2 | Gaps: | 7 |

US-09-809-545a-2 (1-203) x US-08-935-450-10 (1-914)

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QY      24 TyrSerProAspPheTyrAlaGlyThrValLeuLeuGlyAlaAsnGlnGlySer 43
      |||
      230 TACAGCCCT-----GCTCGAAACCCCGAGGGGCC 259
QY      44 SerMetTyrSerGlyProSerSerLeuValTyrThrSerAla-MetProGlyPhePro 63
      |||
      260 AGCAGCTACATTAAGAACACACATCTGCTCAAGGCGCATATCCAGACACCCACC 319
QY      63 rProAlaAlaThrAla-----AlaAlaAlaTyrArgGlyAlaHisLeuArgLysArg 81
      |||
      320 GTCAGCAGCTACAGCCCTTCCACAGCCGAGTTACAGCCACCCCTAC---AACAGGG 376
QY      81 yArgThrValTyrAsnThrPheArgAlaAlaAla-ProProProIleProAlaTyrG 101
      |||
      377 GAGGTTCACAGCCAGGGTTACACAGGCCACCGGCTCCACCTCCACACACACCTGCTTACA 436
QY      101 LysGlyValValTyrGlnGlnProValTyrGlyAsnLysLeuGlnGlyTyrAlaAla 121
      |||
      437 AC-----TATGGAGC-----TACGGCGTTACAGAC 463
QY      121 LArgArgTyrAlaGlnProThrProAlaThrAlaAlaTyrSerAspSerTyrGlyAla 141
      |||
      464 CGGCCCCCTATACCCACCGCCGACCCGCCACCGCACAGAGACTAC----- 507
QY      141 rValTyrAlaAlaAspProTyrHisHisThrLeuAlaProAlaProThrTyrGlyValG 161
      |||
      508 -----CCTCAGCCCACTATACCACT 529
QY      161 LysAlaMetAsnAlaPheAlaProLeuThrAspAlaLysThrArgSerHisAlaAspAsp 181
      |||
      530 ATCAGCAGATATGCCAGCAGGGAACCACTATCTACGAACCAAGGGCAGT----- 579
QY      181 aGlyLeuValLeuSerSerLeuGln 189
      |||
      580 --GGCGGCATACTACGGGAACCTACGA 603
```

RESULT 5
US-08-990-823-62
Sequence 62, Application US/08990823D
Patent No. 6228371
GENERAL INFORMATION:
APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
FILE REFERENCE: 49086
CURRENT APPLICATION NUMBER: US/08/990,823D
CURRENT FILING DATE: 1997-12-15
EARLIER APPLICATION NUMBER: US 96/10375
EARLIER FILING DATE: 1996-06-14
EARLIER APPLICATION NUMBER: 60/000,254
EARLIER FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patentl Ver. 2.0
SEQ ID NO 62
LENGTH: 821
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis


```

QY 140 -----GlyArgValTyrAlaAlaAspProTyrHisHis----- 150
DB 655 GGTGGCTGGGGCGCCGAGAGCCGACGTGGCGC-----CATGTGCG 699
QY 151 -----ThrLeuAlaProAlaProThrTyrGly 159
DB 700 CATGACCCGAACTGAGCCCTGAGCAATGTTGGCTTCACCCCGCGGTTCGGT 759
QY 160 ValGlyAlaMetAsnAlaPheAlaProLeuThrAspAlaLysThrArgSerHisAlaAsp 179
DB 760 GCTGGAATCTCTGACAGCGGTTCATGCGGGTACGACACCGCGGTGTATGATGACATCGCGAC 819

RESULT 7
US-09-103-840A-2
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

Alignment Scores:
Pred. No.: 6.01e+04 Length: 4403765
Score: 97.50 Matches: 66
Percent Similarity: 30.91% Conservative: 19
Best Local Similarity: 24.00% Mismatches: 95
Query Match: 8.98% Indels: 96
Gaps: 12
DB: 3

US-09-809-545A-2 (1-203) x US-09-103-840A-2 (1-4403765)
1 MetThrAsnLysLysAlaValAsnProTyrThrAsnGlyTTrpLysLeuAsnProValVal 20
DB 4237678 ATGGCGGACGAGCTGTGGCCGAGCCGCAATGCGCGCATGTGCAACCGGTTCGG 4237737
QY 21 GlyAlaValAlaTyrSerProAspPheTyrAlaGlyThrValLeuLeuGlyScnAlaAsnGln 40
DB 4237738 GGGCAGGCGTTCGAGCAGCGACCGCTGGGGGTATGATCCCTCGGCTTCAAAACC 4237797
QY 41 Gln-----GlySerSerMetTyrSerGlyPro-----SerSerLeuValTyr 54
DB 4237798 GAGGGCGGTGGCGGAGCACTCAAGTCCGACCGGTGGTCTCCAAACCCGCGGTGTCAC 4237857
QY 55 ThrSerAlaMetProGlyPheProTyrProAlaAlaThrAlaAlaAlaLysTyrArgGly 74
DB 4237858 TCCGATGCGTTCGCGCAACCAACCGACGCGCATACGACGTCGCGGCGACCGCGGA 4237917
QY 75 AlaHisLeuArgGlyArgGlyThrValTyrAsnThrPheArgAlaAlaAlaPro--- 93
DB 4237918 -----GGGAAGGCGCGGTGGGATCAACGGGTTCGACACGCGCGTTCGCGTTC 4237965
QY 94 -----ProProPheProAlaProAlaTyrGly----- 101
DB 4237966 GGATTGGACCGCGGACGTCACCGGATGATGGCGACGTACGGGAGAACAACTGCGCGCC 4238025
QY 102 -----GlyValValTyrGlnGluPro----- 108

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DB 4238026 ACGGACCACTGGCGCTGATACAGTACCGCCCGGACCGGACCGCGCTGGTGGTG 4238085
QY 109 -----ValTyrGlyAsn 112
DB 4238086 GTTTCGCGCGCGCGCCATCTGCTCTACAGAGACGAGCGGATTCATCTACAGCCAG 4238145
QY 113 LysLeu-----LeuGlnGlyGlyTyrAlaAlaLysTyrArgTyrAlaGlnProThrProAlaThr 131
DB 4238146 TCCCTGAACCTGCAGTG-GGG-----GTCACCGCGCGGACGCGCGCATCAGCACT 4238198
QY 132 AlaAlaAlaTyrSerAspSerTyr----- 139
DB 4238199 GGGGACGATATTCCGATGACATGACGACCGCAACCGCGGTGGCGCATCTGCGGTTC 4238258
QY 140 -----GlyArgValTyrAlaAlaAspProTyrHisHis----- 150
DB 4238259 GGTGGCTGGGGCGCGCGGACGCGACGCTGGCGG-----CATGTGCGC 4238303
QY 151 -----ThrLeuAlaProAlaProThrTyrGly 159
DB 4238304 CTATGACCCGAACTGAGCCCTGAGCAATGTTGGCTTCACCCCGCGGTTCGGT 4238363
QY 160 ValGlyAlaMetAsnAlaPheAlaProLeuThrAspAlaLysThrArgSerHisAlaAsp 179
DB 4238364 GCTGGAATCTCTGACAGCGGTTCATGCGGGTACGACGACCGGTGTGATGACATGCGCAC 4238423
QY 180 AspValGlyLeuValLeuSerLeuGlnAlaSerIleTyrGln 194
DB 4238424 CGCAGCAACTT-----CCCTGCGCAGCGACCGTTCGGA 4238459

RESULT 8
US-09-103-840A-1
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.: 6.02e+04 Length: 4411529
Score: 97.50 Matches: 66
Percent Similarity: 30.91% Conservative: 19
Best Local Similarity: 24.00% Mismatches: 95
Query Match: 8.98% Indels: 96
Gaps: 12
DB: 3

US-09-809-545A-2 (1-203) x US-09-103-840A-1 (1-4411529)
1 MetThrAsnLysLysAlaValAsnProTyrThrAsnGlyTTrpLysLeuAsnProValVal 20
DB 4245432 ATGGCGGACGAGCTGTGGCCGAGCCGCAATGCGCGCATGTGCAACCGGTTCGG 4245491
QY 21 GlyAlaValAlaTyrSerProAspPheTyrAlaGlyThrValLeuLeuGlyScnAlaAsnGln 40
DB 4245492 GGGCAGGCGTTCGAGCAGCGACCGCGGTGGTATGATCCCTCGGCTTCAAAACC 4245551
QY 41 Gln-----GlySerSerMetTyrSerGlyPro-----SerSerLeuValTyr 54

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Db 4245552 GAGGCGCTGGCGGAGCACTCAAGTCCGAGCCGGTGTCTCCAAACCGCGGCTGTCAAC 4245611
Oy 55 ThersalameTProGlyPheProTyrProAlaIleThraIleAlaIleAlaIleTyrArgGly 74
Db 4245612 TCCCATGCTGTCGCCCAACAACCCACAGCCGCCATCACCGCATCCGGGGAGACCGCGCGA 4245671
Oy 75 AlahIleuArGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaIlePro--- 93
Db 4245672 -----GGGAAGGCGCGGTCCGGATCAACGGGTGCGACAGCGGCGCTGCCGTTC 4245719
Oy 94 -----ProProIleProAlaTyrGly----- 101
Db 4245720 GGATTGACCCGCACTACCCCGGTGATGGGAGCTACGGGAGAACACACCTGGCGCC 4245779
Oy 102 -----GlyValTyrGlnIlePro----- 108
Db 4245780 ACGGCACTGGCGCTGTACACTTACCGCCCGGACCGCGGACCGCGCTGTGTG 4245839
Oy 109 -----ValTyrGlyAsn 112
Db 4245840 GTTTCGCGCGCGCGCCATCTGCTCTACAGAGAGAGCGCGATTCATCTACGGCGAG 4245899
Oy 113 LysIleu---LeuGlnGlyGlyTyrAlaIleTyrArgTyrAlaGlnProThrProAlaThr 131
Db 4245900 TCCCTGAAACTGCACTG-666-----CGTCACGCGCGCGAGCGCGCATCCAGCACT 4245952
Oy 132 AlahIleuArGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaIlePro--- 139
Db 4245953 GGGCAGGATATTTCGATCGACATCGGACCGCAACCGCGCGGCAATCGCGGTTTC 4246012
Oy 140 -----GlyArgValTyrAlaIleAspProTyrHisHis----- 150
Db 4246013 GCTGGCTGGCGCGCGCGAGCGCGACGTGGCGC-----CATTTGTCG 4246057
Oy 151 -----ThrIleuAlaProAlaProThrTyrGly 159
Db 4246058 CTATGACCCGCACTGAGCCCTGAGCAATGTTCCCTTCACCCCGCGGTTCCGCT 4246117
Oy 160 ValGlyAlaIleAlaIleAlaIlePheAlaIlePheAlaIleTyrArgSerHisAlaAsp 179
Db 4246118 GCTGGAATCTCTGAGCGGTTGATCGGTCAGCAGACCGGTTGATGACATCGCGAC 4246177
Oy 180 AspAlaGlyLeuValIleuSerSerLeuGlnAlaIleSerIleTyrGln 194
Db 4246178 CGCAGCAACTT-----CCCTGCGCAGCAGCAGCTTTCCGA 4246213

RESULT 9
-08-195-152-1
Sequence 1, Application US/08195152
Patent No. 5679541
GENERAL INFORMATION:
APPLICANT: Bonini, Nancy M.
APPLICANT: Lelerson, William M.
APPLICANT: Benzer, Seymour
TITLE OF INVENTION: PROGRAMMED CELL DEATH ANTAGONIST
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,152
FILING DATE: 14-FEB-1994
```

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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Treacartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-59551/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3231 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
US-08-195-152-1

Alignment Scores:
Pred. No.: 5.2 Length: 3231
Score: 56.00 Matches: 45
Percent Similarity: 37.57% Conservative: 23
Best Local Similarity: 24.86% Mismatches: 63
Query Match: 8.84% Indels: 51
DB: 1 Gaps: 6

US-09-809-545a-2 (1-203) x US-08-195-152-1 (1-3231)

Oy 42 GlySerSerMetTyr-----SerGlyProSerSerIleu 52
Db 1062 GGATCCAAATTGTATGGGCTGACGCTCGGCCGCAATCCGTGACGAGGAGGAGCGTGGG 1121
Oy 53 ValTyrThrSerAlaMetProGlyPheProTyrProAlaIleAlaIleAlaIleTyr 72
Db 1122 GTCAACTCTTTCGCACTG------GCAGGCGCAGCAGCGCGCTTAC 1163
Oy 73 ArgGlyAlaHisIleuArGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaIle 92
Db 1164 GACGGCAAACT-----GACTACTACTACTACACACACATGACAGATACAG 1211
Oy 93 ProProProIleProAlaTyrGlyValValTyrGlnIleProValTyrGlyAsn 112
Db 1212 CCGCGCGCTCTCTACTCGGATACGGAATCTTATGCGGCGGACGCGGCGAG 1271
Oy 113 LysIleuGlnGlyGlyTyrAlaIleTyrArgTyrAlaGlnProThrProAlaThrAla 132
Db 1272 GCCAAGATGGAACCGGAGCGCGAGCTGGCGGCTCTTACTTACGCCCATGATGCC 1331
Oy 133 AlahIleu----- 134
Db 1332 GCCAGCGCAACAACATCGCACTGACAGCTCCGTACCGCGGCTACACAACTTC 1391
Oy 135 -----TyrSerAspSerTyrGlyArgValTyrAlaAlaAsp 146
Db 1392 GGGCAGCAGACTACGGCGGCTACTACACAGACAGATGACCACTATTACAGTCGGCC 1451
Oy 147 ProTyrHisThrIleuAlaIleProAlaPro-----ThrTyrGlyValGly--- 161
Db 1452 AACACTACCTACCGGTATGCTGCTCGCCAGCTCGAGTGGAGTGCATGGACATGCTTC 1511
Oy 162 AlahIleuAlaIleAlaIlePheAlaIlePheAlaIleTyrArgSerHisAlaAspVal 181
Db 1512 CATGTGGCGGCTCTGGAATCTCTCCGAGAGTCCACGACACCCACTC- GACGAGGCC 1570
Oy 182 Gly 182
Db 1571 GGT 1573

RESULT 10
US-09-103-840A-2/c
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
```



```

1  APPLICANT: WHITE, Owen R.
2  APPLICANT: FRASER, Claire M.
3  APPLICANT: VENTER, John C.
4  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
5  TITLE OF INVENTION: TUBERCULOSIS
6  FILE REFERENCE: 24366-20007.00
7  CURRENT APPLICATION NUMBER: US/09/103,840A
8  CURRENT FILING DATE: 1998-06-24
9  NUMBER OF SEQ. ID NOS: 2
10 SOFTWARE: PatentIn Ver. 2.1
11 SEQ ID NO 2
12
13 LENGTH: 4403765
14
15 TYPE: DNA
16
17 ORGANISM: Mycobacterium tuberculosis
18 FEATURE:
19 OTHER INFORMATION: CDC 1551
20 OTHER INFORMATION: "n" bases at various positions throughout the sequence
21 OTHER INFORMATION: represent a, t, c or g
22 US-09-103-840A-2

```

| | |
|------------------------|----------|
| Alignment Scores: | |
| Pred. No.: | 1.16e+05 |
| Score: | 94.50 |
| Percent Similarity: | 42.26% |
| Best Local Similarity: | 29.17% |
| Query Match: | 8.70% |
| DB: | 3 |
| | 8 |
| Length: | 4403765 |
| Matches: | 49 |
| Conservative: | 22 |
| Mismatches: | 68 |
| Indels: | 31 |
| Gaps: | 8 |

US-09-809-545A-2 (1-203) x US-09-103-840A-2 (1-4403765)

11 ThrAsnGlyTTrpIysLeuAsnProValValGlyAlaValTyrSerProAspPheTyrAla 30

Db 991136 ACAATGACGCGTGTGTCAATCCTCTACTGCGGGGGGTGGGACCT--GCATATCAG 99

31 GlyThrValLeuLeucysGlnAlaAsnGlnGlnGlySerSerMetTyrSerGlyProSer 500

5310/3 GAGACCCGAAATGCTTTGGAGCCCGCGGACGAGAAATGCCCGACCTGGCCGACACCAATCG 99

[illegible][illegible][illegible]

0x 82 -----AraThrValTvr-----AsnThrPheAraIaaI 91

990899 ACGATGTGCCGACAAGTTCCTCGGCTATATACCAAGCCAGGTGC -TGCGTATTTC 99

91 aaIaProProProIleProAlaTyrGlyGlyValValTyrGlnGluProValTyrGln 11

Db 990840 GGGCGCAGCGCGGCCCGCCAGCCATA-GCCGGGGCGTCGATTGCAGCCGCGAGCGAGTTAGG 99

111 YASNYSLEULENGINGLY---GLTYRALALATYRARGTYRALAGINPROTHRPROAL 13

Db 990781 CGGT--GTGTACCAAGCATTGTTATGCGGCATGACGTACGCC-----99

130 a t n r a l a a l a t y r i s e r a s p s e r t y r g l y a r g i n a l t y r a l a a l a a s p r o t y n h i s h 15

530 / 50 -----GCGCCTGGCCGGGTATATGTCACAGGCACGGTCTCGAGAGCCACCGCATCGCGCGCGGCCG 99

[illegible]

Result 11

US-09-343-011B-3
: Sequence 3: Application US/09343011B

; Patent No. 6300473
; GENERAL INFORMATION:

```

; APPLICANT: Stéphane Richard
; TITLE OF INVENTION: SLM-1 AND SLM-2; NOVEL

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: TITLE OF INVENTION: SAM68-LIKE MAMMALIAN PROTEINS
: FILE REFERENCE: A32561
: CURRENT APPLICATION NUMBER: US/09/343,011B
: PRIOR FILING DATE: 2001-05-11
: PRIOR APPLICATION NUMBER: CA 2265271
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 2368
: TYPE: DNA
: ORGANISM: Mus musculus
: US-09-343-011B-3

Alignment Scores:
Sred. No.: 5.4 Length: 2368
Score: 94.00 Matches: 54
Percent Similarity: 36.93% Conservative: 11
Best Local Similarity: 30.68% Mismatches: 51
Query Match: 8.65% Indels: 60
DB: 4 Gaps: 12

```

US-09-809-545A-2 (1-203) x US-09-343-011B-3 (1-2368)

Qy 73 ArgGlyAlaHisLeuArgGlyArgGlyValArgThrValTyrAsnThrPhe----- 88

Db 1673 CGGGGCGGAGTATTAGCGAGCGGGGTACGAATTAATCTCCACAGCTCCATCAAGGGGC 1732

89 ArgAlaAlaAlaProProProIleProAlaTyrGly

Db 1733 CGTGGCGGTGCTGTTCCACACCACCACCTGGACGAGGTGTGCTTACCCCTGG--- 1789

QY 109 ValTyrGlyAsnLysLeuLeuGlnGly----- 117

Db 1790 -----GGGACCACTGTGACCCCGTGAGCCTCTTCCAGTGCCCCCAATAGCAGAGGTTTC 1843

QY 118-----GlyTyrAlaAla-----TyrArgTyrAlaGlnProThr 128
||| ||||| ||||| ||| |||

DD 1044 CCCACACCTCGAGCCCGGGGACCGCAGTACCAAGGATACAGA--GCACCCCCACCT 1300

[illegible]

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145 A)abcbDrcmTtT-----UicUicmbhTouA)adrcA)adrcmTb----- 157

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Db 1961 GACCAGCCTTATGAGGCTTATGATATAGCTACGTGACCCCAACAAAGTGTGCTGAA 2020

158 -----TyrGlyValGly-----AlaMetAsnAlaPheAlaProLeuThr 170

Db 2021 TACTATGACTACGGTCATGGAGTAACGAGAGATGCCCTACGACAGCTACGCACACAGAGCAA 2080

171 AspaLaLysThrArgSerHisLaAspaSpValGlyLeuValLeuSerSerLeuGlnAla 190

Db 2081 TGGGCCACACTCGC-----TCCAGCCTGAAGGCA 2110

QY 191 -----SerIeTyrGInGIyTYrAsnArpPheAlaProTyr 203

Db 2111 CCACCAACAAGTCAAGCCAGAGGGGATAC---AGGGAGCACCCTTAT 2155

RESULT 12
US-08-804-227C-1/c

Sequence 1, Application US/0680422/C
Patent No. 5876991

APPLICANT: Dehoff, Bradley S.

APPLICANT: Rosteck, Paul R., Jr.
ADDRESSEE: Sutton, Kimberly I.

```

; TITLE OF INVENTION: POLYKERIDE SYNTHASE GENES
; NUMBER OF SEQUENCES: 15

```

;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: THOMAS G. PLANT 1501
;


```

: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2371 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 25..1992
: US-08-343-443B-1

Alignment Scores:
Pred. No.: 7.61 Length: 2371
Score: 92.50 Matches: 48
Percent Similarity: 33.72% Conservative: 10
Best Local Similarity: 27.91% Mismatches: 73
Query Match: 8.52% Indels: 41
DB: 2 Gaps: 9

US-09-809-545a-2 (1-203) x US-08-343-443B-1 (1-2371)
QY 29 TyrAlaGlyThrValLeuLeuCysGlnAla---AsnGlnGluGlySerSerMetTyrSer 47
Db 109 TATGCACAGACACC-----CAGCATATGGGCACAAAGCTATGGAACCTATGCA 159
QY 48 GlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAlaThr 67
Db 160 CAGCCCACTGATGTCACTATACCCAGGCTCAGACCACTCAACCTATGGGCGACGCC 219
QY 68 AlaAlaAlaAlaTyrArgGlyAlaHisLeuArgGlyArgGlyTyrThrValTyrAsnThr 87
Db 220 TATGCAACTCTCTAT-----GGACAGCCTCCCACTGCTATATCTACT 261
QY 88 PheArgAlaAlaAlaProProProProIleProAlaTyrGlyValValTyrGlnGlu 107
Db 262 -----CCAACTGCCCCCAG-----GCATACAGCCAG 288
QY 108 ProValTyrGlyAsnLysLeuLeuGlnGlyTyrAlaAlaTyrArgTyrAlaGlnPro 127
Db 289 CCGTCCAGGGGTAT-----GGCAGCTGCTCTATATGATACACACACGCT 333
QY 128 ThrProAlaThrAlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspPro 147
Db 334 ACAGTCACCCACCCAGGCC-----TCCTATGACGCTCACTCT 372
QY 148 TyrHisHisThrLeuAlaProAlaProThrTyrGlyValGlyAlaMetAsnAlaPheAla 167
Db 373 GCATATGGCAGCTCAGCTGCTTATCCAGCCTATGGGCGAG-----CAG 414
QY 168 ProLeuThrAspAlaLysThrArgSerHisAlaAspAspValGlyLeuValLeuSerSer 187
Db 415 CCAGCAGCCACTGCACCTACAGACCCGAGATGGAACAAGCCCACTGAGACTAGTCAA 474
QY 188 LeuGlnAlaSerIleTyrGlnGlyTyrAsnArg 199
Db 475 CCTCAATCTAGC-----ACAGGGGGTTACACACAG 504

RESULT 14
US-08-437-027-18
: Sequence 18, Application US/08437027
: Patent No. 5670317
: GENERAL INFORMATION:
: APPLICANT: Landany1, Marc
: APPLICANT: Gerald, William
: TITLE OF INVENTION: A DIAGNOSTIC TEST FOR TEST FOR THE DESMOPLASTIC
: TITLE OF INVENTION: SMALL ROUND CELL TUMOR
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooper & Dunham LLP
: STREET: 1185 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.

```

```

: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/437,027
: FILING DATE:
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: White, John P
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 46416/JPW/CCA
: TELEPHONE: 212-278-0400
: TELEFAX: 212-391-0525
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2412 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: US-08-437-027-18

Alignment Scores:
Pred. No.: 7.79 Length: 2412
Score: 92.50 Matches: 48
Percent Similarity: 33.72% Conservative: 10
Best Local Similarity: 27.91% Mismatches: 73
Query Match: 8.52% Indels: 41
DB: 1 Gaps: 9

US-09-809-545a-2 (1-203) x US-08-437-027-18 (1-2412)
QY 29 TyrAlaGlyThrValLeuLeuCysGlnAla---AsnGlnGluGlySerSerMetTyrSer 47
Db 109 TATGCACAGACACC-----CAGCATATGGGCACAAAGCTATGGAACCTATGCA 159
QY 48 GlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAlaThr 67
Db 160 CAGCCCACTGATGTCACTATACCCAGGCTCAGACCACTCAACCTATGGGCGACGCC 219
QY 68 AlaAlaAlaAlaTyrArgGlyAlaHisLeuArgGlyArgGlyTyrThrValTyrAsnThr 87
Db 220 TATGCAACTCTCTAT-----GGACAGCCTCCCACTGCTATATCTACT 261
QY 88 PheArgAlaAlaAlaProProProProIleProAlaTyrGlyValValTyrGlnGlu 107
Db 262 -----CCAACTGCCCCCAG-----GCATACAGCCAG 288
QY 108 ProValTyrGlyAsnLysLeuLeuGlnGlyTyrAlaAlaTyrArgTyrAlaGlnPro 127
Db 289 CCGTCCAGGGGTAT-----GGCAGCTGCTCTATATGATACACACACGCT 333
QY 128 ThrProAlaThrAlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspPro 147
Db 334 ACAGTCACCCACCCAGGCC-----TCCTATGACGCTCACTCT 372
QY 148 TyrHisHisThrLeuAlaProAlaProThrTyrGlyValGlyAlaMetAsnAlaPheAla 167
Db 373 GCATATGGCAGCTCAGCTGCTTATCCAGCCTATGGGCGAG-----CAG 414
QY 168 ProLeuThrAspAlaLysThrArgSerHisAlaAspAspValGlyLeuValLeuSerSer 187
Db 415 CCAGCAGCCACTGCACCTACAGACCCGAGATGGAACAAGCCCACTGAGACTAGTCAA 474
QY 188 LeuGlnAlaSerIleTyrGlnGlyTyrAsnArg 199
Db 475 CCTCAATCTAGC-----ACAGGGGGTTACACACAG 504

RESULT 15

```


GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 25, 2003, 11:57:25 : Search time 169 Seconds
(without alignments)
2990.335 Million cell updates/sec

Title: US-09-809-545A-2
Perfect score: 1086
Sequence: 1 MTMKKAVNPYTGKLNPNV.....VLSLQASIVCGGYNRPAPY 203

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1678620 segs, 1244745471 residues
Total number of hits satisfying chosen parameters: 3357240

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV-xlp
-MODEL-frame+ p2n model -DB-Published,Applications_VA -OFMT-fastap -SUFFIX-rnpb -MINMATCH=0.1
-LOOFCU=0 -LOOEXT=0 -UNITS-bits -START=1 -END=1 -MATRIX-blosum62
-TRANS-numa40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pcr -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER-US09809545 -CGCN 1.1 85 -runat 25092003.111105.22925
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSEPLock=100
-LONLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCNUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match Length | DB ID | Description |
|------------|-------|--------------|-------|------------------|
| 1 | 1086 | 100.0 | 1340 | US-09-809-545A-1 |

| 2 | 955 | 87.9 | 2372 | 9 | US-09-794-591-1 | Sequence 1, Appl1 |
|----|-------|------|---------|----|---------------------|--------------------|
| 3 | 500.5 | 46.1 | 1843 | 11 | US-09-919-039-266 | Sequence 266, App |
| 4 | 467.5 | 43.0 | 1506 | 11 | US-10-359-785-5 | Sequence 5, Appl1 |
| 5 | 116 | 10.7 | 11447 | 12 | US-10-301-822-25 | Sequence 25, Appl |
| 6 | 116 | 10.7 | 11447 | 14 | US-10-177-293-60 | Sequence 60, Appl |
| 7 | 116 | 10.7 | 11560 | 14 | US-10-177-293-62 | Sequence 62, Appl |
| 8 | 116 | 10.7 | 11657 | 14 | US-10-198-846-11039 | Sequence 11039, A |
| 9 | 108.5 | 10.0 | 6930 | 13 | US-10-098-841-226 | Sequence 226, App |
| 10 | 107 | 9.9 | 895 | 9 | US-09-770-445-681 | Sequence 481, App |
| 11 | 102.5 | 9.4 | 1089 | 14 | US-10-156-761-2655 | Sequence 2655, App |
| 12 | 102.5 | 9.4 | 9025608 | 14 | US-10-156-761-1 | Sequence 1, Appl1 |
| 13 | 99.5 | 9.2 | 5643 | 12 | US-10-012-952A-43 | Sequence 43, Appl |
| 14 | 99 | 9.1 | 60 | 12 | US-09-908-975-7420 | Sequence 7420, App |
| 15 | 99 | 9.1 | 464 | 13 | US-10-027-632-18118 | Sequence 18118, A |
| 16 | 98.5 | 9.1 | 821 | 10 | US-09-996-634-62 | Sequence 62, Appl |
| 17 | 98.5 | 9.1 | 821 | 11 | US-09-997-182-62 | Sequence 62, Appl |
| 18 | 98.5 | 9.1 | 821 | 11 | US-09-997-181-62 | Sequence 62, Appl |
| 19 | 97.5 | 9.0 | 2658 | 9 | US-09-815-242-4035 | Sequence 4035, App |
| 20 | 97.5 | 9.0 | 3285 | 10 | US-09-712-363-143 | Sequence 143, App |
| 21 | 96 | 8.8 | 3231 | 8 | US-08-754-311B-1 | Sequence 1, Appl1 |
| 22 | 95.5 | 8.8 | 9025608 | 14 | US-10-156-761-1 | Sequence 1, Appl1 |
| 23 | 94 | 8.7 | 657 | 10 | US-09-974-300-1655 | Sequence 1655, App |
| 24 | 93 | 8.6 | 2076 | 14 | US-10-156-761-7099 | Sequence 7099, App |
| 25 | 92.5 | 8.5 | 699 | 13 | US-10-027-632-24830 | Sequence 24830, A |
| 26 | 92.5 | 8.5 | 699 | 13 | US-10-027-632-24831 | Sequence 24831, A |
| 27 | 92.5 | 8.5 | 699 | 13 | US-10-027-632-24832 | Sequence 24832, A |
| 28 | 92.5 | 8.5 | 2273 | 10 | US-09-822-830A-410 | Sequence 410, App |
| 29 | 92.5 | 8.5 | 2390 | 10 | US-09-880-107-3769 | Sequence 3769, App |
| 30 | 92.5 | 8.5 | 2390 | 12 | US-09-873-319-717 | Sequence 717, App |
| 31 | 92.5 | 8.5 | 2390 | 12 | US-09-960-706-1081 | Sequence 1081, App |
| 32 | 92.5 | 8.5 | 2760 | 14 | US-10-128-714-7387 | Sequence 7387, App |
| 33 | 92.5 | 8.5 | 2902 | 14 | US-10-128-714-6387 | Sequence 6387, App |
| 34 | 92.5 | 8.5 | 4514 | 14 | US-10-128-714-5387 | Sequence 5387, App |
| 35 | 92.5 | 8.5 | 4902 | 14 | US-10-128-714-5387 | Sequence 5387, App |
| 36 | 92 | 8.5 | 53522 | 11 | US-09-904-968A-1 | Sequence 1, Appl1 |
| 37 | 91.5 | 8.4 | 969 | 14 | US-10-125-635A-452 | Sequence 452, App |
| 38 | 91 | 8.4 | 3673 | 14 | US-10-157-031-332 | Sequence 332, App |
| 39 | 90.5 | 8.3 | 1443 | 14 | US-10-156-761-4462 | Sequence 4462, App |
| 40 | 90.5 | 8.3 | 1743 | 10 | US-09-887-576-788 | Sequence 788, App |
| 41 | 90.5 | 8.3 | 1869 | 14 | US-10-156-761-3570 | Sequence 3570, App |
| 42 | 90.5 | 8.3 | 2804 | 12 | US-10-023-782A-3 | Sequence 3, Appl1 |
| 43 | 90.5 | 8.3 | 4340 | 14 | US-10-198-846-12986 | Sequence 12986, A |
| 44 | 90 | 8.3 | 466 | 11 | US-09-918-995-8298 | Sequence 8298, App |
| 45 | 90 | 8.3 | 1782 | 10 | US-09-938-842A-1143 | Sequence 1143, App |

ALIGNMENTS

RESULT 1
US-09-809-545A-1
Sequence 1, Application US/09809545A1
Patent No. US20020110804A1
GENERAL INFORMATION:
APPLICANT: Stanton, Lawrence W.
APPLICANT: White, R. Tyler
TITLE OF INVENTION: SECRETED FACTORS
FILE REFERENCE: SCIOS 017A
CURRENT APPLICATION NUMBER: US/09/809, 545A
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1340
TYPE: DNA
ORGANISM: Rattus norvegicus
US-09-809-545A-1

Alignment Scores:

| Pred. No.: | 4.32e-117 | Length: | 1340 |
|------------------------|-----------|---------------|------|
| Score: | 1086.00 | Matches: | 203 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |

| DB: | 10 | Gaps: | 0 |
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| US-09-809-545A-2 (1-203) x US-09-809-545A-1 (1-1340) | | | |
| Qy | 1 | MethrAsnLysAlaValAsnProTyrThrAsnGlyTyrPylsLeuAsnProValVal | 20 |
| | | | |
| Db | 535 | ATGACTATAAAAAAGCGCGTGAACCCCTACACCAATGGCTGGAAATTAAATCCAACTTGTG | 594 |
| Qy | 21 | GLyAlaValIYrSerProAspPheTyrAlaGlyThrValLleuLeuCysGlnAlaAsnGln | 40 |
| | | | |
| Db | 595 | GGCCGGGCTCTACAGCCCGGACCTTCATTCAGGACGAGGTGTGTGGCCAGGCCAAACAG | 654 |
| Qy | 41 | GLuGlySerSerMetTyrSerGlyProSerSerLeuValIYrThrSerAlaMetProGly | 60 |
| | | | |
| Db | 655 | GAGGAGTCTTCATCATGTACAGTGGCCCCAGTTCACTTGATATATCTTGCAATGGCTTGGC | 714 |
| Qy | 61 | PheProTyrProAlaAlaThrAlaAlaAlaAlaIaTyrArgGlyAlaHisLeuArgLysArg | 80 |
| | | | |
| Db | 715 | TTTCCATATCCGGGGCGCCACTGCTGTACACTGCTGATACGAGGGGCTCACCTTGGAGCGGT | 774 |
| Qy | 81 | GLyArgThrValIYrAsnThrPheArgAlaAlaAlaAlaProProProIleProAlaTyr | 100 |
| | | | |
| Db | 775 | GGTGGCACCGGTGTCAACACCCCTTCAGACCTGGGGCCCCACCCCAATCCCGGCTTAT | 834 |
| Qy | 101 | GLyGlyValIaIYrGlnGluProValIYrGlyAsnLysLeuLeuGlnGlyIYrAla | 120 |
| | | | |
| Db | 835 | GGCGGAGTAGTGTATCAAGAGCCAGGTGTATGGCAATTAATGTCTACAGGGGTGTATACCT | 894 |
| Qy | 121 | AlaTyrArgTyrAlaGlnProThrProAlaThrAlaAlaIaTyrSerAspSerTyrGly | 140 |
| | | | |
| Db | 895 | GCAATACCGCTACGCCACGCCACCCCTGCCACTGGCTGCTACAGTAGACGTTACGGA | 954 |
| Qy | 141 | ArgValIYrAlaAlaAspProTyrHisHisThrLeuAlaProAlaProThrTyrGlyAla | 160 |
| | | | |
| Db | 955 | CGAGCTTATGTGTGGCGACCCCTTACCACACACACTTGTCTCCAGCCCCACCTACGGCGTT | 1014 |
| Qy | 161 | GLyAlaMetAsnAlaPheAlaProLeuThrAspAlaLysTyrArgSerHisAlaAspAsp | 180 |
| | | | |
| Db | 1015 | GGTGCATGATGCTTTGGCCCTCTGACCGATGCCAAGACTAGAGCCATGCTGATAT | 1074 |
| Qy | 181 | ValGlyLeuValLleuSerSerLeuGlnAlaSerIleTyrGlnGlyIYrAsnArgPhe | 200 |
| | | | |
| Db | 1075 | GTGGGTCTCGCTTCTTCTTCATTCAGCGCTAGTATATGCCAAAGGGGATACAAACCGTTTT | 1134 |
| Qy | 201 | AlaProTyr | 203 |
| | | | |
| Db | 1135 | GCTCCATAT | 1143 |
| RESULT 2 | | | |
| US-09-794-591-1 | | | |
| : Sequence 1, Application US/09794591 | | | |
| : Patent No. US20010018198A1 | | | |
| : GENERAL INFORMATION: | | | |
| : APPLICANT: Pulsat, Stefan M. | | | |
| : APPLICANT: Shibata, Hiroki | | | |
| : TITLE OF INVENTION: Nucleic Acids Encoded Ataxin-2 Binding Proteins, | | | |
| : FILE REFERENCE: CE 3093 | | | |
| : CURRENT APPLICATION NUMBER: US/09/794,591 | | | |
| : CURRENT FILING DATE: 2001-02-26 | | | |
| : PRIOR APPLICATION NUMBER: 09/145,391 | | | |
| : PRIOR FILING DATE: 1998-09-01 | | | |
| : NUMBER OF SEQ ID NOS: 2 | | | |
| : SOFTWARE: PatentIn Ver. 2.0 | | | |
| : SEQ ID NO 1 | | | |
| : LENGTH: 2372 | | | |
| : TYPE: DNA | | | |
| : ORGANISM: Homo sapiens | | | |
| : FEATURE: | | | |
| : NAME/KEY: CDS | | | |
| : LOCATION: (987)..(1979) | | | |
| US-09-794-591-1 | | | |

| Alignment Scores: | 1.72e-101 | Length: | 2372 |
|------------------------|-----------|---------------|------|
| Pred. No.: | 955.00 | Matches: | 189 |
| Score.: | 86.94% | Conservative: | 4 |
| Best Local Similarity: | 85.14% | Mismatches: | 9 |
| Query Match: | 87.94% | Indels: | 21 |
| DB: | 9 | Gaps: | 2 |

| US-09-809-545A-2 (1-203) x US-09-794-591-1 (1-2372) |
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| QY 1 MetpRrAsnLysLysAlaValAsnProthrYrhrAsnGlyTrpLysLeuAsnProValVal 20 |
| Db 1572 ATGCAAAATTAATAAGACCCGTCAACCTTATACAAATGGCTGGAATATGAATCCAGTTGTG 16311 |
| QY 21 GAlaValAlTYrSerProAspPheTYrAlaGlyThrValLeuLeuCYsGlnAlaAsnGln 40 |
| Db 1632 GGTGAGCTPACAGTCCGCAATTCATGACAGACGGTCCGTGTGTGGCAGCCACACAG 16911 |
| QY 41 GluGlySerSerMetTYrSerGlyProSerSerLeuValTYrThrSerAlaMetProGly 60 |
| Db 1692 GAGGATCTTCCATGATACAGTACGTCGCCCGCCAGTTCATGATATACCTTGCATCCAGGC 17511 |
| QY 61 PheProTYrProAlaAlaThrAlaAlaAlaAlaAlaTYrArgGlyAlaHisLeuArgGlyArg 80 |
| Db 1752 TTCCCGATCCAGCAGCCGACCGCGCGCCCTTACCGAGGGGGCGACCTCGAGGCCGC 18111 |
| QY 81 GlyArGThrValTYrAsnThrPheArGAlaAlaAlaProProProPoleProAlaTYr 100 |
| Db 1812 GGTGCGACCGTGTACAAACACTTACAGGGCGCGGGGCCGCCCGATCCGGGCTAC 18711 |
| QY 101 GlyGlyValValTYr-GlnGluProValTYrGlyAsnLysLeuLeuGlnGlyTYrAl 120 |
| Db 1872 GCGCGTGTCTTACCCAGGATGATTTATGATGTCAGAC--ATTATGCTGCTATGTC 19281 |
| QY 120 aAlaTYrArGTYrAlaGlnProthrProAlaThAlaAlaAlaTYrSerAspSer----- 138 |
| Db 1929 TGCATACCGCTACGCCACGCTTACCCCTGCCACATGCCCTGCTCAAGTGCAG-AAATC 19871 |
| QY 139 -----TYrGlyArgVa 142 |
| Db 1988 AGTTCGCTCTTGTGCACAGATGAATTTCTTGAACACCTCTGCAGTTACGAGCAGT 20471 |
| QY 142 lTYrAlaAlaAspProTYrHisHisThrLeuAlaProAlaProthrTYrGlyValGlyAl 162 |
| Db 2048 TTATGCTGCGCCACCCCTACACACAGCAGCCTGTCTCCAGCCCCCAGCTACGGCGTTGGTC 21071 |
| QY 162 aMetAsnAlaPheAlaProLeuThrAspAlaLysThrArgSerHisAlaAspAspValGl 182 |
| Db 2108 CATGATGCTTTTGACACTTGTGACTGATGACCAAGACTAGAGCCATGCTGATGATGGG 21671 |
| QY 182 yLeuValLeuSerSerLeuGlnAlaSerIleTYrGlnGlyGlyTYrAsnArgPheAlaPr 202 |
| Db 2168 TCTGTTCTTCTTCATTCATGACGCGTAGATATACGAGGGGAGTAAACGTTTGGTCC 22271 |
| QY 202 CTyr 203 |
| Db 2228 ATAC 2231 |

| RESULT 3 |
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| US-09-919-039-266 |
| ; Sequence 266, Application US/09919039 |
| ; Publication No. US20030108871A1 |
| ; GENERAL INFORMATION: |
| ; APPLICANT: Kaser, Matthew R. |
| ; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES |
| ; FILE REFERENCE: PA-0035 US |
| ; CURRENT APPLICATION NUMBER: US/09/919, 039 |
| ; CURRENT FILING DATE: 2002-09-09 |
| ; PRIOR APPLICATION NUMBER: 60/222,113 |
| ; PRIOR FILING DATE: 2000-07-28 |
| ; NUMBER OF SEQ ID NOS: 401 |
| ; SOFTWARE: PERL Program |
| ; SEQ ID NO 266 |

: LENGTH: 1843
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : NAME/KEY: misc_feature
 : OTHER INFORMATION: Incyte ID No. US20030108871A1 253783.3
 : FEATURE:
 : NAME/KEY: unsure
 : LOCATION: 1824
 : OTHER INFORMATION: a, t, c, g, or other
 : US-09-919-039-266

Alignment Scores:
 Pred. No.: 1.32e-48 Length: 1843
 Score: 500.50 Matches: 105
 Percent Similarity: 52.61% Conservative: 6
 Best Local Similarity: 49.76% Mismatches: 23
 Query Match: 46.09% Indels: 77
 DB: 11 Gaps: 5

US-09-809-545a-2 (1-203) x US-09-919-039-266 (1-1843)

QY 1 MetThrsAnlysAlaValaAsnProTyrThrAsnGlyTrrplysLeuAsnProVal 20
 DB 1228 ATGACCACCAAGAGAGAGCGGGAACCCCTACACCAAGCGCTGAAGCTAAATCCAGTGTG 1287
 QY 21 G1ValaValTyrSerProAspPheTyrAlaGlyThrValLeuLeucysGlnAlaAsnGln 40
 DB 1288 GCGGCACTTACGCGGCTGAAATCTATGACGTGACG----- 1323
 QY 41 GluGlySerSerMetTyrSerGlyProSerSerLeuValTyrThrSerAlaMetProGly 60
 DB 1324 -----GGG 1326
 QY 61 PheProTyrProAlaAlaThrAlaAlaAlaAlaTyrArgGlyAlaHisLeuArgGlyArg 80
 DB 1327 TTCCTCCATCCACACACCGGCGACGCTGCTACCGGCGGCGCACATCTTCGCGGCGCG 1386
 QY 81 G1AArgThrValTyrAsnThrPheArgAlaAlaAlaProProProProIleProAlaTyr 100
 DB 1387 GCGCGGCGCGCTGTATATATACATTTCCGGCTGCGCGCACCGCCACCCCATCCGACTTAC 1446
 QY 101 GlyGly----- 102
 DB 1447 GGAGCGGACTGAGCAAAACGTTGTTAAATGCCAGTCCCATGGCGGGCGTGGCACCG 1506
 QY 102 ----- 102
 DB 1507 TGGCCCTCCCTCCTCAGACAGACCGGCGGCTACCCACCTCTCCAGCGTTCCCA 1566
 QY 103 -----ValValTyrGlnGluProValTyrGlyAsnLys 113
 DB 1567 CCACCTTCTTGTCCGTTTGGCTTCAGAGGCTGTGTATCAGATGATTTTATGTGTGAG 1626
 QY 114 LeuLeuGlnGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThrAlaAla 133
 DB 1627 ---ATTATGAGAGCTACGACGAGCTACAGTACGCTCAGCCGCT---GGAAGGCGGCGCA 1680
 QY 134 AlaTyrSerAspSerTyrGlyArgValTyr---AlaAlaAspProTyrHisHisThrLeu 152
 DB 1681 GCGTACAGCGACAGTTACGCGCAGAGTCTACGACAGTCCGACCCGTTACATCACACCATC 1740
 QY 153 AlaProAlaProThrTyrGlyValGlyAlaMet 163
 DB 1741 GCGCGCGCGCGACCTACAGCATTTGCAACCATG 1773

RESULT 4
 US-10-359-385-5
 : Sequence 5, Application US/10359385
 : Publication No. US20030143622A1
 : GENERAL INFORMATION:
 : APPLICANT: Bandman, Olga
 : APPLICANT: Tang, Y. Tom

: APPLICANT: Corley, Neil C.
 : APPLICANT: Guejler, Karl J.
 : APPLICANT: Lu, Aina
 : APPLICANT: Baughn, Mariah R.
 : TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
 : FILE REFERENCE: PE-0611 US
 : CURRENT APPLICATION NUMBER: US/10/359,385
 : CURRENT FILING DATE: 2003-02-05
 : PRIOR APPLICATION NUMBER: US/09/176,657
 : PRIOR FILING DATE: 1998-10-21
 : NUMBER OF SEQ ID NOS: 9
 : SOFTWARE: PERL Program
 : SEQ ID NO 5
 : LENGTH: 1506
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : OTHER INFORMATION: 1250374
 : US-10-359-385-5

Alignment Scores:
 Pred. No.: 7.19e-45 Length: 1506
 Score: 467.50 Matches: 107
 Percent Similarity: 56.48% Conservative: 15
 Best Local Similarity: 49.54% Mismatches: 39
 Query Match: 43.05% Indels: 56
 DB: 12 Gaps: 8

US-09-809-545a-2 (1-203) x US-10-359-385-5 (1-1506)

QY 1 MetThrsAnlysAlaValaAsnProTyrThrAsnGlyTrrplysLeuAsnProVal 20
 DB 768 ATGACCACCAAGAGAGTGTGTCACACCATATGCAAAATGTGGAAATTAAGCCAGTAGTT 827
 QY 21 G1ValaValTyrSerProAspPheTyrAlaGlyThrValLeuLeucysGlnAlaAsn--- 39
 DB 828 GGAGCTGTATATGTCGCGAGTTATATGACATCCAGCTTTCACAGATGTGTCCCTTA 887
 QY 40 ---GluGlySerSerMetTyrSerGlyProSerSerLeu-----ValTyrThrSer 56
 DB 888 GGCATATGTCACAGTGCCTTATCAGGAAGGGGGGTTCACACTTACATCTCTTA 947
 QY 57 AlaMetProGlyPheProTyrPro---AlaAlaThrAlaAlaAlaAlaTyrArgGlyAla 75
 DB 948 ATGATTCCTGCGCTTCCTTACCTTACCTACGACGACGACCGCGCTTCAAGAGAGCC 1007
 QY 76 HisLeuArgGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaAlaProProPro 95
 DB 1008 CATTTGAGGGGAGAGGGCGGACAGTATATGTGACAGTCCGA---CGGTAACCTCCACA 1064
 QY 96 ProIleProAlaTyrGlyValValTyrGlnGluProValTyrGlyAsnLysLeuLeu 115
 DB 1065 GCCATCCCGCCCATCC----- 1081
 QY 116 GlnGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr----- 131
 DB 1082 AGGGGTGATATGACACCTTACATATGACACACCGCTGCTACCAACCGACCGACCGCT 1141
 QY 132 -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspPro 147
 DB 1142 GCTGACGCGCTCAGCCGCTTACGTACGTATATGCGGTATGCGGTGTATACACAGCGACCC 1201
 QY 148 TyrHisHisThrLeuAlaProAlaProThrTyrGlyValGlyAlaMetAsnAlaPheAla 167
 DB 1202 TAC---CATGCCCTTCCCGCTGCGGTACGTATGAGAGTGGCGCTGTG----- 1246
 QY 168 ProLeuThrAspAlaLysThrArgSerHisAlaAspAspValGlyLeuValLeuSerSer 187
 DB 1246 ----- 1246
 QY 188 LeuGlnAlaSerLeTyrGlnGlnGlyTyrAsnArgPheAlaProTyr 203
 DB 1247 -----GCGAGTTTATACGAGGTGCTTACAGCGCATTTGCCCTTAC 1288

[illegible]

```

RESULT 7
US-10-17-293--62
: Sequence 62, Application US/10177293
: Publication NO. US20030124128A1
GENERAL INFORMATION:
: APPLICANT: Lillie, James
: APPLICANT: Gialt, Karen
: APPLICANT: Zhao, Xunlei
: APPLICANT: Gannavarpu, Manjula
: APPLICANT: Kamatkar, Shubhangi
: APPLICANT: Mertens, Maureen
: APPLICANT: Myer, Vic
: APPLICANT: Wang, Youzhen
: APPLICANT: Xu, Yongyao
: APPLICANT: Hoersch, Sebastian
: APPLICANT: Monahan, John
: APPLICANT: Meyers, Rachel E.
: APPLICANT: Bast Jr., Robert C.
: APPLICANT: Hortobagyi, Gabriel N.
: APPLICANT: Puztal, Lajos
: APPLICANT: Meric, Funda
: APPLICANT: Sahlin, Aysegul
: APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT
FILE REFERENCE: MRI-038
CURRENT APPLICATION NUMBER: US/10/177,293
PRIOR FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US/60/299,887
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/xxx,xxx
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SOFTWARE: FastSeq for Windows Version 4.0

```

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: SEQ_ID NO 62
: LENGTH: 11560
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 10981
: OTHER INFORMATION: n = A,T,C or G
US-10-177-293-62

Alignment Scores:
Pred. No.:          0.00992      Length:      11560
Score:              116.00      Matches:      45
Percent Similarity: 34.08%      Conservative: 16
Best Local Similarity: 25.14%      Mismatches:  54
Query Match:        10.68%      Indels:      64
DB:                  14          Gaps:         8

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US-09-809-545A-2 (1-203) x US-10-177-293-62 (1-11560)
OY      50 SerSerLeuValIlyTrThSerAlaMetProGlyPheProTyRProAlaIalaThAlaIala 69
       : ::::: ::::: ||| ||||| |||
Db      6345 AACATGTAAATCTGCACGCCCCCTGCACCACTCACACTCATAT---AAAATTACGTGTATT 6401
OY      70 AlaIaIyTArg-----GjAlaHisLeuArGjIyArTGjIyArGThVal----- 84
       ||| ||| ||| ||||| ||| ||||| |||||
Db      6402 GCTGTTTATGAAGATGGAGATGCGGCCCATCTTAACAGGAATAATGGAGAACACTGTGGGACTC 6466
OY      85 -----TyrAsnThrPheaArgAlaIala 92
       ||| ||| ||||| |||
Db      6462 CTTCCTCCTCAGAACATACACATCTCTGACGAATGGTATACAAATTCACAGGCTGCTCGG 6522
OY      93 ProProProProlleProAlaTyGjIyAlaValIyTrGInglProValTyGIyLysn 112
       ||| ||| ||| ||| ::::: ||||| |||
Db      6522 GATCCTTCACCCTTCTCCAGTTCTTGGAATATAAANAATAGATATAAAGCCAGTGGTCCAT 6581
OY      113 LysLeuleugln-----GjVgLyTyraIalaIyTArgTyraIaglProthrPro 129
       ::::: ||| ||| ::::: |||
Db      6582 GAGCCCATGGAAGCCTTGTGTGGAGAAATGACATCATATFACCTTA----- 6628
OY      130 AlaThrIalaIalaIyTyrSerAspSerTyGIyArGjValTYrAlaIalaAspProTyRhIs 149
       6626 ----- 6628
OY      150 HisThrIleaIaProAlaProThTyTcyIyAlaGjAlaMetAsnAlaPheIa----- 167
       ||| ||| ||| ::::: ||||| |||
Db      6627 CACAATTCATCAATCCCAGCACCCATCCACATGTG-----AATGTTATGCTCAATAT 6677
OY      168 -----ProLeuthrAspAlaLysThrArgSerHisAlaAspArgVal 181
       ||| ||||| ||||| |||
Db      6678 GATTCGTGACATCATGTGCCCTTTCAGACATCAAGGACTACA----- 6719
OY      182 GlyLeuValLeuSerSerLeuGlnAlaSerIleTyTrGInglGjIyTyrAsnArgPhe 200
       ||| ||| ::::: ||||| ||| ||||| |||
Db      6720 ---TTATATTAAATGTAAACAGANTCTGAAAACTTACACAGATTGGGTGGGATACATTC 6773

RESULT 8
US-10-198-846-11039
; Sequence 11039, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lille, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198, 846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306, 220
; PRIOR FILING DATE: 2001-07-18
```

```

: NUMBER OF SEQ ID NOS: 14084
: SOFTWARE: fastseq for windows version 4.0
: SEQ ID NO 11039
: LENGTH: 11657
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1, 2, 3, 4, 11656, 11657
: OTHER INFORMATION: n = A,T,C or G
US-10-198-846-11039

Alignment Scores:
Pred. No.: 0.01 Length: 11657
Score: 116.00 Matches: 45
Percent Similarity: 34.08% Conservative: 16
Best Local Similarity: 25.14% Mismatches: 54
Query Match: 10.68% Indels: 64
DB: 14 Gaps: 8

-09-809-545A-2 (1-203) x US-10-198-846-11039 (1-11657)

QY 50 SerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaIaIaIaIa 69
DB 6398 AACAAATGTAATCTGACGCCCTGCACCTGCACCTCCATAT---AAAATTACTGTATT 6454
QY 70 AlaAlaTyrArg-----GlyAlaHisLeuArgGlyArgGlyArgGlyArgGly 84
DB 6455 GCTGTATTATGAAGATGAGAGATGAGTGGCCATTAACAGAAATGGAAGAACTGTGGGACTC 6514
QY 85 -----TyrAsnThrPheArgAlaAlaAla 92
DB 6515 CTTCCTCTCAGACATACACATCTCTGACGAATGATTAACAAATTCAGGGTGTCTGG 6574
QY 93 ProProProIleProAlaTyrGlyGlyValTyrGlyGlyGlyGlyGlyGlyGly 112
DB 6575 GATCCTTCACCTCTCCACCTCTTGTGATTAATAATAGTATTAAGCCAGTGGTCCANT 6634
QY 113 LysLeuLeuGln-----GlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrPro 129
DB 6635 GAGCCCATGGAAGCCTTGTGTGAGAAATGACATCATATACCTTA----- 6679
QY 130 AlaThrAlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspProThrHis 149
DB 6679 ----- 6679
QY 150 HisThrLeuAlaProAlaProThrTyrGlyValGlyAlaMetAsnAlaPheAla----- 167
DB 6680 CACATCTTCATCCACGACGACGACCTACGATG-----AATGTTTATCTCAATAT 6730
QY 168 -----ProLeuThrAspAlaLysThrArgSerHisAlaAspAspVal 181
DB 6731 GATTCTGACATCAGTGTCCCTTTCGACAGATCAAGGACATACA----- 6772
QY 182 GlyLeuValLeuSerSerLeuGlnAlaSerIleTyrGlnGlyGlyTyrAsnArgPhe 200
DB 6773 ---TTATATTAAATGTAACAGATCTGAAAACCTTACGAGATTGGGTGATACATTC 6826

RESULT 9
US-10-098-841-226
: Sequence 226, Application US/10098841
: Publication No. US20020197679A1
: GENERAL INFORMATION:
: APPLICANT: Tang, Y. Tom
: APPLICANT: Liu, Chenghua
: APPLICANT: Asundi, Vinod
: APPLICANT: Xu, Chongjun
: APPLICANT: Zhou, Ping
: APPLICANT: Ma, Yundong
: APPLICANT: Wang, Jian-Rui
: APPLICANT: Zhao, Qiang A.
: APPLICANT: Ren, Feiyun
: APPLICANT: Chen, Rui-hong

```

```

: APPLICANT: Wang, Dunrui
: APPLICANT: Wang, Zhiwei
: APPLICANT: Wehrman, Tom
: APPLICANT: Zhang, Jie
: APPLICANT: Qian, Xiaohong B.
: APPLICANT: Drmanac, Radoje T.
: TITLE OF INVENTION: No. US20020197679A1el Nucleic Acids and
: FILE REFERENCE: 784CIP2
: CURRENT APPLICATION NUMBER: US/10/098,841
: PRIOR FILING DATE: 2002-03-13
: PRIOR APPLICATION NUMBER: 09/598,042
: PRIOR FILING DATE: 2000-06-20
: PRIOR APPLICATION NUMBER: 09/552,317
: PRIOR FILING DATE: 2000-04-25
: PRIOR APPLICATION NUMBER: 09/488,725
: PRIOR FILING DATE: 2000-01-21
: NUMBER OF SEQ ID NOS: 331
: SOFTWARE: PC_FL_genes Version 1.0
: SEQ ID NO 226
: LENGTH: 6930
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (234)..(968)
US-10-098-841-226

Alignment Scores:
Pred. No.: 0.0386 Length: 6930
Score: 108.50 Matches: 56
Percent Similarity: 35.85% Conservative: 20
Best Local Similarity: 26.42% Mismatches: 67
Query Match: 9.99% Indels: 69
DB: 13 Gaps: 12

US-09-809-545A-2 (1-203) x US-10-098-841-226 (1-6930)

QY 6 AlaValAsnProTyrThrAsnGlyTyrPylsLeuAsnProValValAlaValTyrSer 25
DB 336 GCCATCAATCCC-----AGCTGTACCCACCAATATAGCCCATATATGCT 380
QY 26 ProAspPhe-----TyrAlaGlyThrValLeuLeuGlyGlnAlaAsn 39
DB 381 CCAGAGTTCACGTTCTGTCGATTCACCTTATGCA---ACTGCTGATGAAACAGGCCCTGG 437
QY 40 GlnGlnGlySerSer-----MetTyrSerGly 48
DB 438 CCACAGAACTGCTTCTCTGTCGACGACGACGACCTTCCACCTCCAGTGGACGCGG 497
QY 49 ProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAlaThrAla 68
DB 498 ACCGAGAACCGAACTTACCAAGCATCTCTGCGCTTCAGATAT-----ACTGCG 548
QY 69 AlaAlaAlaTyrArgGlyAlaHisLeuArgGlyArgGlyArgThrValTyrAsnThrPhe 88
DB 549 GGGACACCATACAG-----GTCCACCGACCGCAG 578
QY 89 ArgAlaAlaAlaProProProIleProAlaTyrGlyGlyValValTyrGlnGlnPro 108
DB 579 AGTACACTGCTCCACCCCTCTACTCCCATCACCAAC-----CCCTATCAGAGCGG 632
QY 109 ValTyr-----GlyAsnLysLeuGlnGlyGlyTyrAla 120
DB 633 ATGTATCAATACAGAAAGTGCCTACCCGACGAGATCTGTATGCGCAGGAGGCTAC--- 689
QY 121 AlaTyrArgTyrAlaGlnProThrProAlaThrAlaAlaTyrSerAspSerTyrGly 140
DB 690 -----TACACACACCG----- 701
QY 141 ArgValTyrAlaAlaAspProTyr-----HisHisThrLeuAlaProAlaProThrTyr 158
DB 702 ---GTGTATGCTGCCAGCTCTATGTATCATCCACACACGAGGTCGTCCAGCCCAAC--- 755

```

QY 159 GlyValGlyAlaMetAsnAlaPheAlaProLeuThrAspAlaLysThrArgSerHisAla 178
Db 756 -----ACGATTCCTCTGCTGCTATGTACCAGCACCTGTGGCCCGGAGGACCAACGCT 809
QY 179 AspAspValGlyLeuValLeuSerSerLeuGlnAla 190
Db 810 GTGGCATGGGCGATGTGGCAGGACACCATGGCA 845

RESULT 10
US-09-770-445-481/c
Sequence 481, Application US/09770445
Patent No. US20020023281A1
GENERAL INFORMATION:
APPLICANT: Goriach, Jorm
APPLICANT: An, Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Rameaka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Matthew, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Moessner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Krickler, Maja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILE REFERENCE: 20230US (PARA-012PRV)
CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 481
LENGTH: 895
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-770-445-481

Alignment Scores:
ed. No.: 0.00422 Length: 895
Score: 107.00 Matches: 52
Percent Similarity: 36.60% Conservative: 19
Best Local Similarity: 26.80% Mismatches: 63
Query Match: 9.85% Indels: 60
DB: 9 Gaps: 11

US-09-809-545A-2 (1-203) x US-09-770-445-481 (1-895)
QY 42 GlySerSerMetGlyrSerGlyProSerSerLeuValGlyThrSerAlaMetProGlyPhe 61
Db 869 GGTGATGTGCTTACCAAGTCCA-----ACACCGAGCAGCAGCCGTATGTTAT 825
QY 62 ---ProGlyProAlaAla-----ThrAlaAlaAlaAlaAlaGlyAla 75
Db 824 GGTTCACACCGAGGAGCATGTGTATGTTCACTCCAGGACCATCGTATGTTCA 765
QY 76 HisLeuArgGlyArg-----GlyArgThrValGly 85
Db 764 AACGTGGCTGACACAGCAATATGTTATGCATCAAGTGGCGCTACGACAACTAT 705
QY 86 AsnThrPheArgAlaAlaAlaPro-----ProProProLe 97
Db 704 CCTTCATATAGCTCTGCGAGCAGCATGTGATGTTATATGTTACAAACGACGAGT 645

QY 98 ---ProAlaGlyr-----GlyGlyValValGlyGlnPro 108
Db 644 GCCCGAGCTTATGAGCAGACAGCGGTGCACGACCTTGTGTGCAACAACTTCAGCT 585
QY 109 ValTyrGlyAsnLysLeuGlnGlyGlyAlaAlaAlaGlyArgGlyAlaGlnProThr 128
Db 584 GGGTACGGGCAAGTACCTCCAGACGGGTGGCTATGTTGTTCCCTCCACACAGCGGCT 525
QY 129 ProAlaThrAlaAlaAlaTyrSerAsp---SerTyrGlyArgValTyrAlaAlaAspPro 147
Db 524 TATGTATATACCCCGGCTCAAGCAATGGAACATATGGA-----TCAATGGCTCTCAG 471
QY 148 TyrHisHisThrLeuAlaProAlaProThrTyrGlyAlaGlyAlaMetAsnAlaPheAla 167
Db 470 TAT-----CTTAGCTATGAGGATGGAAAGCATGCAATAGCT 432
QY 168 ProLeuThrAspAlaLysThrArgSerHisAlaAspValGlyLeuValLeuSerSer 187
Db 431 GCACCTACTGGCCCAACCGCTATATCC----- 405
QY 188 LeuGlnAlaSerTleTyrGlnGlyGlyTyrAsnArgPheAla 201
Db 404 ---CAGACTGCACCTCTCCAGGCGGCTATGAGCAATCAGCA 366

RESULT 11
US-10-156-761-2655
Sequence 2655, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 2655
LENGTH: 1089
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1089)
US-10-156-761-2655

Alignment Scores:
Pred. No.: 0.0181 Length: 1089
Score: 102.50 Matches: 48
Percent Similarity: 40.00% Conservative: 18
Best Local Similarity: 29.09% Mismatches: 55
Query Match: 9.44% Indels: 44
DB: 14 Gaps: 10

US-09-809-545A-2 (1-203) x US-10-156-761-2655 (1-1089)
QY 59 ProGlyPheProTyrProAlaAlaAlaThrAlaAlaAlaAlaGlyArgGlyAlaAlaLeuArg 78
Db 636 CTTGGGGGCGCTTACGAGCAGGAGGAGCGGCTGCGAGACAGCAGGAGCGGAGCTAGCT 695
QY 79 GlyArgGlyArgThrValGlyAsnThr---PheArgAlaAlaAlaProPro----- 94
Db 696 GCGCGGTCTGGCGGAGCGTCCGCAACACCGCCGACGAGCGGCTGGGACGCGGCGGAGCGGCT 755

```

OY      95 -----ProProlleProAlaTYrGlyGlyValValTYrGlnGlnProValTYrGlyAs 112
          ||| ||||| |||||
Db      756 CCAGGCCCCCTAGATCCCGGCT-----CAGCCGCACTAC----- 789
OY      112 nLysLeuLcGlnGlnGlyTYrAlaAlaTYrArgTYrAlaGlnProThrPro----- 129
          ||| ||||| ||||| ||| ||| |||||
Db      790 -----GGCGGGCAGAGAGCGCTACGCGCAGCAGCAGCAGCAGCCGATCCGTA 836
OY      130 -----AlaThrAlaAlaAlaTYrSerAspSerTYrGlyArgValTYrAlaAlaAspPr 147
          ||| ||||| ||||| ||||| ||||| |||||
Db      837 CGGCTACCAGCAGCAGCTACGCGCAGCAGCAGCAGCGTACGCTACCGACCGCAGCGCGACCC 896
OY      147 oTYrHisHisThrLeuAlaProAlaProThrTYrGlyAlaGlyAlaMetAsnAlaPhe-- 166
          |||| |||| |||| |||| |||| |||||
Db      897 GTAC-----GCCGGGTACCGCAGCAGGCGTACGACGACGACGAGCGCGCTACGA 944
OY      167 -----AlaProLeuThr---AspAlaLysThrArgSerHis 177
Db      945 CCAGAACCCAGCAGCAGGCGTACTCCACCGCAGCAGCAGCAGCAGCGCAGCGCAGCA 1004
          177 s---AlaAspAspValGlyLeu-----ValLeuSerSerLeuGlnAlaSerHis 192
          | ||||| ||||| ||||| ||||| ||||| |||||
Db      1005 CGACCTGGACGACGAGCCACCTCTTCGCACACGACGACATGATCGGAGACAGCTCGGGGC 1064
OY      192 eTYrGlnGlyGly 196
          ||||| |||
Db      1065 CTACGAAACAGGGG 1077

RESULT 12
US-10-156-761-1/c
/ Sequence 1, Application US/10156761
/ Publication No. US20030119018A1
/ GENERAL INFORMATION:
/ APPLICANT: OMURA, SATOSHI
/ APPLICANT: IKEDA, HARUO
/ APPLICANT: ISHIKAWA, JUN
/ APPLICANT: HORIKAWA, HIROSHI
/ APPLICANT: SHIBA, TADAYOSHI
/ APPLICANT: SAKAKI, YOSHIYUKI
/ APPLICANT: HATTORI, MASAHIRA
/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
/ FILER REFERENCE: 249-262
/ CURRENT APPLICATION NUMBER: US/10/156,761
/ CURRENT FILING DATE: 2002-05-29
/ PRIOR APPLICATION NUMBER: JP 2001-204089
/ PRIOR FILING DATE: 2001-05-30
/ PRIOR APPLICATION NUMBER: JP 2001-272697
/ PRIOR FILING DATE: 2001-08-02
/ NUMBER OF SEQ ID NOS: 15109
/
/ SEQ ID NO 1

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Alignment Scores:
Pred. No.:      1.87e+03      Length:      9025608
Score:          102.50        Matches:     48
Percent Similarity: 40.00%    Conservative: 18
Best Local Similarity: 29.09% Mismatches:   55
Query Match:     9.44%       Indels:      44
DB:              14          Gaps:        10

US-09-809-545A-2 (1-203) x US-10-156-761-1 (1-9025608)

Oy      59 ProcllyPheproryrPrroAlaIaLThAlaLaIaLaIaLyArGGLyAlaHisLeuArg 78
         |||||  |||||  |||  |||:::||||  |||
Db      3270608 CcTtGGGCGCCCTTCACGGAGCAGCAAGCGCCGTCCACACACGACGCGCGACTCT 3270549

```

| | | | | |
|----|---------|--|---|-----|
| OY | | 79 | GlyArgGly-ArgThrValTyrAsnThr-----PheArgAlaIleAlaProP----- | 94 |
| Dd | 3270548 | GGCCGGCTGGCGGACCTCGGCACACC-----CGAGCAGCCCTCGCACCGGCCAGACCCC | 32704899 | |
| OY | | 95 | -----ProIleIleProAlaTyrglyglyValvalTyrglnIleProValTyrglyAs | 112 |
| Dd | 3270488 | CCAGGCCCCCTGAGATCCCGGCT-----CAGCGCGAGTAC----- | 32704555 | |
| OY | | 112 | nLysLeuLeuGlnIleGlyTygAlaIalAaTygArgTygAlaGlnProIlePro----- | 129 |
| Dd | 3270454 | -----GGCGGGCAGACGGCTACGCGTACGAGAGACAGACCCCGATCCCTTA | 32704088 | |
| OY | | 130 | -----AlaThrAlaIalaIaIaTyrSerASpSerTyrglyArtyValTygAlaIalaAspr | 147 |
| Dd | 3270407 | CGGCTACCAAGACAGAGTAGGCGCCAGCAGAGACGGCTACGGGTACCAAGCGCAGAGCGCGAACCC | 32703488 | |
| OY | | 147 | OTyrlHisIstlThreulaIaprolAlaproThrtYrglyValglValaIleMetlsnalape-- | 166 |
| Dd | 3270347 | GTCAC-----GCCGGTGACCCCGCAGCAGCGGTACGACCCAGCAGACGAGCGGCTACGA | 32703000 | |
| OY | | 167 | -----AlaProIeuThr-----AspAlaIysThrArgSeriH | 177 |
| Dd | 3270239 | CCAGAACCAGCAGCAGGGGCTACTCCACAGCCGACAGACGACGACATCTCCACGCCGACGGCACA | 3270240 | |
| OY | | 177 | s---AlaspaSpValglLeu-----ValIeuSerIerLeuGlinaISerII | 192 |
| Dd | 3270239 | CGACCTGGAGCAGAGCGCCAGCGCTCTTCGACACACGACCATGATCAGTCGCGAGCAGCTGCGGGC | 32701800 | |
| OY | | 192 | eTyrglnIglyly 196 | |
| Dd | 3270179 | CTACGACACAGGGG 3270167 | | |

```

? TITLE OF INVENTION: Composition and Methods Relating to Prostate Specific Genes and
? FILE REFERENCE: DEX-0263
? CURRENT APPLICATION NUMBER: US/10/012,952A
? PRIORITY FILING DATE: 2001-11-06
? PRIOR APPLICATION NUMBER: US 60/246,039
? PRIOR FILING DATE: 2000-11-06
? NUMBER OF SEQ ID NOS: 248
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 43
? LENGTH: 5643
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (5471)..(5471)
? OTHER INFORMATION: n=a, c, g or t
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (5501)..(5501)
? OTHER INFORMATION: n=a, c, g or t
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (5559)..(5560)
? OTHER INFORMATION: n=a, c, g or t
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (5634)..(5634)
? OTHER INFORMATION: n=a, c, g or t
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (5636)..(5636)
? OTHER INFORMATION: n=a, c, g or t
? US-10-012-952A-43

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 25, 2003, 12:06:55; Search time 49 Seconds
(without alignments)
1333.157 Million cell updates/sec

Title: US-09-809-545a-2_COPY_1_148
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Ygapop 10.0, Ygapext 0.5
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Delop 6.0, Delext 7.0

arched: 569978 segs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|------------------|
| 1 | 674 | 84.7 | 2372 | 3 | US-09-145-391-1 |
| 2 | 379 | 47.6 | 1506 | 3 | US-09-176-657-5 |
| 3 | 379 | 47.6 | 1506 | 4 | US-09-421-299-5 |
| 4 | 93 | 11.7 | 914 | 2 | US-08-935-450-10 |
| 5 | 92.5 | 11.6 | 28958 | 1 | US-08-258-261B-6 |
| 6 | 92.5 | 11.6 | 28958 | 1 | US-08-456-837-6 |
| 7 | 92.5 | 11.6 | 28958 | 1 | US-08-457-342-6 |
| 8 | 92.5 | 11.6 | 28958 | 1 | US-08-457-646A-6 |
| 9 | 92.5 | 11.6 | 28958 | 1 | US-08-458-076A-6 |
| 10 | 92.5 | 11.6 | 28958 | 1 | US-08-764-233A-4 |
| 11 | 92.5 | 11.6 | 28958 | 1 | US-08-457-335A-6 |
| 12 | 92.5 | 11.6 | 28958 | 1 | US-08-729-214-6 |

| | | | | | | |
|----|------|------|---------|---|--------------------|--------------------|
| 13 | 92.5 | 11.6 | 28958 | 3 | US-09-028-934-6 | Sequence 6, Appl1 |
| 14 | 92.5 | 11.6 | 49377 | 1 | US-08-764-233A-1 | Sequence 1, Appl1 |
| 15 | 91 | 11.4 | 821 | 3 | US-08-990-823-62 | Sequence 62, Appl1 |
| 16 | 91 | 11.4 | 821 | 4 | US-09-477-135A-62 | Sequence 62, Appl1 |
| 17 | 91 | 11.4 | 1896 | 4 | US-09-343-011B-4 | Sequence 4, Appl1 |
| 18 | 89.5 | 11.2 | 4403765 | 3 | US-09-103-860A-2 | Sequence 2, Appl1 |
| 19 | 89.5 | 11.2 | 441529 | 3 | US-09-103-860A-1 | Sequence 1, Appl1 |
| 20 | 87.5 | 11.0 | 3231 | 1 | US-08-195-152-1 | Sequence 1, Appl1 |
| 21 | 86.5 | 10.9 | 4403765 | 3 | US-09-103-860A-2 | Sequence 2, Appl1 |
| 22 | 86.5 | 10.9 | 4411529 | 3 | US-09-103-860A-1 | Sequence 1, Appl1 |
| 23 | 85.5 | 10.7 | 1140 | 3 | US-09-023-173-4 | Sequence 4, Appl1 |
| 24 | 85.5 | 10.7 | 2208 | 4 | US-09-620-312D-502 | Sequence 502, App |
| 25 | 85 | 10.7 | 53526 | 3 | US-08-658-136-2 | Sequence 2, Appl1 |
| 26 | 85 | 10.7 | 53577 | 3 | US-08-658-136-1 | Sequence 16, Appl1 |
| 27 | 84.5 | 10.6 | 1462 | 1 | US-08-552-142A-16 | Sequence 16, Appl1 |
| 28 | 84.5 | 10.6 | 1494 | 3 | US-09-255-502-1 | Sequence 1, Appl1 |
| 29 | 84.5 | 10.6 | 1496 | 6 | RE34606-1 | Patent No. RE34,60 |
| 30 | 84.5 | 10.6 | 1497 | 1 | US-08-322-677A-6 | Sequence 6, Appl1 |
| 31 | 84.5 | 10.6 | 1497 | 1 | US-08-322-676-6 | Sequence 6, Appl1 |
| 32 | 84.5 | 10.6 | 1497 | 3 | US-08-898-218-6 | Sequence 6, Appl1 |
| 33 | 84.5 | 10.6 | 1497 | 3 | US-08-848-793-6 | Sequence 6, Appl1 |
| 34 | 84.5 | 10.6 | 1497 | 4 | US-09-445-270-1 | Sequence 1, Appl1 |
| 35 | 84.5 | 10.6 | 1497 | 4 | US-09-178-173A-1 | Sequence 1, Appl1 |
| 36 | 84.5 | 10.6 | 1497 | 4 | US-08-322-678-6 | Sequence 6, Appl1 |
| 37 | 84.5 | 10.6 | 1497 | 6 | 5472855-1 | Patent No. 5472855 |
| 38 | 84.5 | 10.6 | 1513 | 4 | US-09-178-155-1 | Sequence 1, Appl1 |
| 39 | 84.5 | 10.6 | 1513 | 1 | US-08-069-863-1 | Sequence 1, Appl1 |
| 40 | 84.5 | 10.6 | 1668 | 1 | US-08-309-069-1 | Sequence 1, Appl1 |
| 41 | 84.5 | 10.6 | 1668 | 1 | US-08-562-833-1 | Sequence 1, Appl1 |
| 42 | 84.5 | 10.6 | 1668 | 4 | US-09-659-749-1 | Sequence 1, Appl1 |
| 43 | 84.5 | 10.6 | 1668 | 4 | US-09-672-105-1 | Sequence 1, Appl1 |
| 44 | 84.5 | 10.6 | 1868 | 5 | PCT-US95-05520-1 | Sequence 1, Appl1 |
| 45 | 83.5 | 10.5 | 1352 | 1 | US-08-552-142A-10 | Sequence 10, Appl1 |

ALIGNMENTS

RESULT 1
US-09-145-391-1
; Sequence 1, Application US/09145391
; Patent No. 6194171
; GENERAL INFORMATION:
; APPLICANT: Pulist, Stefan M.
; APPLICANT: Shibata, Hiroki
; TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
; FILE REFERENCE: CE 3093
; CURRENT APPLICATION NUMBER: US/09/145,391
; CURRENT FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (987)..(1979)
US-09-145-391-1

Alignment Scores:

Pred. No.: 4.26e-59 Length: 2372
Score: 674.00 Matches: 136
Percent Similarity: 83.238 Conservative: 3
Best Local Similarity: 81.448 Mismatches: 8
Query Match: 84.67% Indels: 21
DB: Gaps: 2

US-09-809-545A-2_COPY_1_148 (1-148) x US-09-145-391-1 (1-2372)

OY 1 MetTnAsnLysAlaValAsnProTyrTnAsnGlyTnPLysLeuAsnProValVal 20
DB 1572 ATGACAAATATAAGACCTCAACCTTATACAAATATGCTGGAATTTGATTCAGTTGTG 1631

OY 21 G1yAlaValTySerProAspPheTyrAlaGlyThrValLeuLeuCySGlnAlaAsnGln 40
|||||
Db 1632 GGTCACACTTACAGATCCCGAATTCTATGACAGGCGGTGCTGTCACAGGCCAACAG 1691
OY 41 GluGlySerSerMetTyrSerGlyProSerSerLeuValTyrThrSerAlaMetProGly 60
|||||
Db 1692 GAGGGAATCTTCCAGTACAGAGGCCCGCCAGTTCACTTATATACTTCTGCAATCCAGCC 1751
OY 61 PheProTyrProAlaIleThrAlaAlaAlaAlaIleTyrArgGlyAlaHisLeuArgGlyArg 80
|||||
Db 1752 TTCCCGATTCACAGACCGCCGCGCCGCTACCGAGGGCGCCACTGCGAGGCCGC 1811
OY 81 GlyArgThrValTyrAsnThrPheArgAlaAlaAlaProProProIleProAlaTyr 100
|||||
Db 1812 GGTCACACGCTGTACACACCTTCAGGGCGCGCGGCCGCCGCCGATCCGAGCTAC 1871
OY 101 G1yGlyValValTyr-GlnGluProValTyrGlyAsnLeuLeuGlnGlyTyrAl 120
1872 GCGCGTGTGTTCACCGAGATGATTTATGTCGACAG-ATTTATGCTGTTATGC 1928
OY 120 AlaTyrArgTyrAlaGlnProThrProAlaThrAlaAlaIleTyrSerAspSer----- 138
|||||
Db 1929 TGCATACCGCTACGCCACGCTACCTGCGCTGCTTACAGTGACAG-AAATC 1987
OY 139 -----TyrglyArgVal 142
Db 1988 AGTTCGTCTTCGTTGACAGAGATGAATTTCTGTACACCTCTGACAGTTACGAGCAGT 2047
OY 142 ITyrAlaAlaAspProTyr 148
Db 2048 TTATGCTGCCGACCCCTAC 2066

RESULT 2

US-09-176-657-5
: Sequence 5, Application US/09176657
: Patent No. 6020164
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Tang, Y. Tom
: APPLICANT: Corley, Neil C.
: APPLICANT: Guegler, Karl J.
: APPLICANT: Lu, Alina
: APPLICANT: Baughn, Mariah R.
: TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
: FILE REFERENCE: PF-0611 US
: CURRENT APPLICATION NUMBER: US/09/176, 657
: CURRENT FILING DATE: 1998-10-21
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PERL Program
: SEQ ID NO 5
: LENGTH: 1506
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE: -
: OTHER INFORMATION: 1250374
US-09-176-657-5

Alignment Scores:

Pred. No.: 1,97e-29 Length: 1506
Score: 379.00 Matches: 86
Percent Similarity: 59.63% Conservative: 10
Best Local Similarity: 53.42% Mismatches: 37
Query Match: 47.61% Indels: 29
DB: Gaps: 6

US-09-809-545a-2_COPY_1_148 (1-148) x US-09-176-657-5 (1-1506)

OY 1 MetThrAsnLysAlaValAsnProTyrThrAsnGlyTyrPlyLeuAsnProValVal 20
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Db 768 ATGACCAATAGAAGATGTCACACCATATGCAAAATGTTGAATTAAGCCAGTATGTT 827
OY 21 G1yAlaValTySerProAspPheTyrAlaGlyThrValLeuLeuCySGlnAlaAsn--- 39

Db 828 GGACCTCATATGCTCCGCGAGTTATATGACAGCATCCAGCTTTCAGCAGATGTGTCCCTA 887
OY 40 ---GlnGlySerSerMetTyrSerGlyProSerSerLeu-----ValTyrThrSer 56
Db 888 GGCATATGACAGCAGTCCCTATACAGAGAGGGGGTATCAACTTACATTCCTTTA 947
OY 57 AlaMetProGlyPheProTyrPro--AlaAlaThrAlaAlaAlaTyrArgGlyAla 75
Db 948 ATCATTCCTGCTCCCTTACCTTACCGCCACGACCGAGCGCTTTCAGAGAGACC 1007
OY 76 HisLeuArgGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaAlaProPro 95
Db 1008 CATTTGAGGGGACAGAGGCGGACGATATGTCAGTCCGA---GGGTAACCTCCACA 1064
OY 96 ProIleProAlaTyrGlyValValTyrGlnGluProValTyrGlyAsnLeuLeu 115
Db 1065 GCCATCCCGCCCTATCC----- 1081
OY 116 GlnGlyValTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr----- 131
Db 1082 AGGGGTGATATGACGCTACAGATATGACAGCCTGCTACTGCAACCGCAGCCAGCCGT 1141
OY 132 -----AlaAlaIleTyrSerAspSerTyrGlyArgValTyrAlaAlaAspPro 147
Db 1142 GCTGACACCGCTGACGCGCTTACAGTACGCGTTATGACAGGGTGTACACAGCCGACC 1201
OY 148 Tyr 148
Db 1202 TAC 1204

RESULT 3

US-09-421-299-5
: Sequence 5, Application US/09421299
: Patent No. 6524579
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Tang, Y. Tom
: APPLICANT: Corley, Neil C.
: APPLICANT: Guegler, Karl J.
: APPLICANT: Lu, Alina
: APPLICANT: Baughn, Mariah R.
: TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
: FILE REFERENCE: PF-0611 US
: CURRENT APPLICATION NUMBER: US/09/421, 299
: CURRENT FILING DATE: 1999-10-20
: EARLIER APPLICATION NUMBER: 09/176, 657
: EARLIER FILING DATE: 1998-10-21
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PERL Program
: SEQ ID NO 5
: LENGTH: 1506
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE: -
: OTHER INFORMATION: 1250374
US-09-421-299-5

Alignment Scores:

Pred. No.: 1,97e-29 Length: 1506
Score: 379.00 Matches: 86
Percent Similarity: 59.63% Conservative: 10
Best Local Similarity: 53.42% Mismatches: 37
Query Match: 47.61% Indels: 29
DB: Gaps: 6

US-09-809-545a-2_COPY_1_148 (1-148) x US-09-421-299-5 (1-1506)

OY 1 MetThrAsnLysAlaValAsnProTyrThrAsnGlyTyrPlyLeuAsnProValVal 20
|||||
Db 768 ATGACCAATAGAAGATGTCACACCATATGCAAAATGTTGAATTAAGCCAGTATGTT 827
OY 21 G1yAlaValTySerProAspPheTyrAlaGlyThrValLeuLeuCySGlnAlaAsn--- 39


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|||||
Db 828 GGAGCTGATATGCTCCGAGATTATGACAGATCCATTTCAGCAGATGTGCTTA 887
Qy 40 ---GlnGlnGlnSerSerMetTyrSerGlyProSerSerLeu-----ValTyrThrSer 56
Db 888 GGCAATGATACACAGTCCCTTACGAGAGAGGGGGTATCAACACTTACATTCCTTTA 947
Qy 57 AlameProGlyPheProTyrPro---AlaAlaThrAlaAlaAlaAlaTyrArgGlyAla 75
Db 948 ATCATTCCTGCTTCCTTCCCTTACCTACTGACAGCCACAGCGAGCGCTTTCAGAGGAGCC 1007
Qy 76 HisLeuArgGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaAlaProPro 95
Db 1008 CATTTGAGGGGAGAGGGGCGGACAGATATGTTGACACTCGCA---GCGTACCTCCACACA 1064
Qy 96 ProIleProAlaTyrGlyValValTyrGlnGlnIleProValTyrGlyAsnLysLeu 115
Db 1065 GCCATCCCGCCCTATCC----- 1081
Qy 116 GlnGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr----- 131
Db 1082 AGGGGTGATATGATGAGCTTACAGATATGACAGCGCTGCTCTGCAACCGCAGCCGCT 1141
Qy 132 -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspPro 147
Db 1142 GCTGACAGCCGCTGACAGCGCTTACAGTACAGTATGACAGGGGTATGACAGCGGATACAGCC 1201
Qy 148 Tyr 148
Db 1202 TAC 1204
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RESULT 4
US-08-935-450-10
: Sequence 10 Application US/08935450
: Patent No. 5977311
: GENERAL INFORMATION:
: APPLICANT: Nandabalan, Krishnan
: APPLICANT: Yang, Meljia
: APPLICANT: Schulz, Vincent
: TITLE OF INVENTION: 53BP2 COMPLEXES
: FILE REFERENCE: 7934-054
: CURRENT APPLICATION NUMBER: US/08/935,450
: CURRENT FILING DATE: 1997-09-23
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 10
: LENGTH: 914
: TYPE: DNA
: ORGANISM: Homo sapiens
US-08-935-450-10
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Alignment Scores:
Pred. No.: 1 Length: 914
Score: 93.00 Matches: 39
Percent Similarity: 41.38% Conservative: 9
Best Local Similarity: 33.62% Mismatches: 42
Query Match: 11.68% Indels: 26
DB: 2 Gaps: 5
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US-09-809-545a-2_COPY_1_148 (1-148) x US-08-935-450-10 (1-914)

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Qy 24 TyrSerProAspPheTyrAlaGlyThrValIleuLeuGlnAlaAsnGlnGlnGlySer 43
Db 230 TACAGCCCT-----GCTGGAAACCCCGCCAGGGGCC 259
Qy 44 SerMetTyrSerGlyProSerSerLeuValTyrThrSerAla-MetProGlyPheProTyr 63
Db 260 AGCAGCTTACATAAGAACACATCCCTGCTCAAGCCCAATACACACCCACCC 319
Qy 63 rProAlaAlaThrAla-----AlaAlaAlaTyrArgGlyAlaHisLeuArgGlyArg 81
Db 320 GTCAGCAGCTACAGCCCTTCCACAGCGGAGTTACAGCCACCAACCCCTAC---AACGAGG 376
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Qy 81 YArgThrValTyrAsnThrPheArgAlaAlaAla-ProProProIleProAlaTyrG 101
Db 377 GAGGTACAGCCAGGGTTACACAGCGCCGCTCCACCTCCACACACAGCTGCTACA 436
Qy 101 lGlyValValTyrGlnGlnIleProValTyrGlyAsnLysLeuGlnGlyTyrAla 121
Db 437 AC-----TATGGAGC-----TACGGCGGTTACANCC 463
Qy 121 lArTyrArgTyrAlaGlnProThrProAlaThrAlaAlaTyr 135
Db 464 CGGCCCCCTATACCCACCGCACCCCGCCACAGACCTAC 507
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RESULT 5
US-08-258-261B-6
: Sequence 6, Application US/08258261B
: Patent No. 5639949
: GENERAL INFORMATION:
: APPLICANT: Schupp, Thomas
: APPLICANT: Beck, James M.
: APPLICANT: Ligon, James Joseph
: APPLICANT: Hill, Dwight Steven
: APPLICANT: Ryals, John Andrew
: APPLICANT: Gaffney, Thomas Deane
: APPLICANT: Lam, Stephen Ting
: APPLICANT: Hammer, Phillip E.
: APPLICANT: Uknes, Scott Joseph
: TITLE OF INVENTION: Genes for the synthesis of
: TITLE OF INVENTION: antipathogenic substances
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Ciba-Geigy Corporation
: STREET: 7 Skyline Drive
: CITY: Hawthorne
: STATE: NY
: COUNTRY: USA
: ZIP: 10532
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/258,261B
: FILING DATE: 08-JUN-1994
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/457,205
: FILING DATE: 01-JUN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Elmer, James Scott
: REGISTRATION NUMBER: 36,129
: REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-8614
: TELEFAX: 919-541-8689
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 28958 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEetical: NO
: ANTI-SENSE: NO
US-08-258-261B-6

Alignment Scores:
Pred. No.: 106 Length: 28958
Score: 92.50 Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 11.62% Indels: 12
DB: 1 Gaps: 4
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US-09-809-545a-2_COPY_1_148 (1-148) x US-08-258-261B-6 (1-28958)
QY 47 SerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAla 66
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Db 10706 AGCGGCTCCTCCGAGATGGGCGATCGCTTCCGCGAGTGAAGCCCATCCGCTGCCA 10765
QY 67 ThrAlaAlaAlaAlaTyr--ArgGlyAlaHis-LeuArgGlyValArgTyrValTyr 85
    ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 10766 CGCTCGCCCTCCGAGACGTGCGAGCGCTCAGCCGCTCAGTCCGCTCGCTGCCA 10825
QY 85 rAsnThrPheArgAlaAlaAlaProProProPheProAlaTyrGlyGlyValTyr 105
    ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 10826 TTCGACG--AGAAGAAGGCCACCTCGCCGCTCCTCGCTCGCGGAGCTCTCTA 10882
QY 105 rGlnGluProValTyrGlyValNlysLeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAl 125
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 10883 CCCGAGGCGCT-----CGCGCTCGACTGGAAGACTCTTGGCGGCTACGCTCC 10933
QY 125 agln-----ProThrProAlaThrAlaAlaAlaTyrSerAspSerTyr 139
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 10934 GCAAGGTCTCCCTCCACCTACCTACCTTCCAGCAGAGCGGCTTGGCTCGACGTCTCA 10993
QY 139 rGlyArgValTyrAlaAlaAspPro 147
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Db 10994 CGGAGGAACGCTTCGAGCTCGCCT 11018

RESULT 6
US-08-456-837-6
: Sequence 6, Application US/08456837
: Patent No. 5643774
: GENERAL INFORMATION:
: APPLICANT: Schupp, Thomas
: APPLICANT: Ligon, James M.
: APPLICANT: Beck, James Joseph
: APPLICANT: Hill, Dwight Steven
: APPLICANT: Ryals, John Andrew
: APPLICANT: Gaffney, Thomas Deane
: APPLICANT: Lam, Stephen Ting
: APPLICANT: Hammer, Phillip E.
: APPLICANT: Uknes, Scott Joseph
: TITLE OF INVENTION: Genes for the synthesis of
: TITLE OF INVENTION: antipathogenic substances
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Ciba-Geigy Corporation
: STREET: 7 Skyline Drive
: CITY: Hawthorne
: STATE: NY
: COUNTRY: USA
: ZIP: 10532
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/456.837
: FILING DATE: 01-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/457,205
: FILING DATE: 01-JUN-1995
: APPLICATION NUMBER: 08/258,261
: FILING DATE: 08-JUN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Elmer, James Scott
: REGISTRATION NUMBER: 36,129
: REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-8614
: TELEFAX: 919-541-8689
: INFORMATION FOR SEQ ID NO: 6:

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: SEQUENCE CHARACTERISTICS:
: LENGTH: 28958 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
US-08-456-837-6

Alignment Scores:
Pred. No.: 106 Length: 28958
Score: 92.50 Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 11.62% Indels: 12
DB: 1 Gaps: 4

US-09-809-545a-2_COPY_1_148 (1-148) x US-08-456-837-6 (1-28958)
QY 47 SerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAla 66
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 10706 AGCGGCTCCTCCGAGATGGGCGATCGCTTCCGCGAGTGAAGCCCATCCGCTGCCA 10765
QY 67 ThrAlaAlaAlaAlaTyr--ArgGlyAlaHis-LeuArgGlyValArgTyrValTyr 85
    ::::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 10766 CGCTCGCCCTCCGAGACGTGCGAGCGCTCAGCCGCTCAGTCCGCTCGCTGCCA 10825
QY 85 rAsnThrPheArgAlaAlaAlaProProProPheProAlaTyrGlyGlyValTyr 105
    ::::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 10826 TTCGACG--AGAAGAAGGCCACCTCGCCGCTCCTCGCTCGCGGAGCTCTCTA 10882
QY 105 rGlnGluProValTyrGlyValNlysLeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAl 125
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 10883 CCCGAGGCGCT-----CGCGCTCGACTGGAAGACTCTTGGCGGCTACGCTCC 10933
QY 125 agln-----ProThrProAlaThrAlaAlaAlaTyrSerAspSerTyr 139
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 10934 GCAAGGTCTCCCTCCACCTACCTACCTTCCAGCAGAGCGGCTTGGCTCGACGTCTCA 10993
QY 139 rGlyArgValTyrAlaAlaAspPro 147
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Db 10994 CGGAGGAACGCTTCGAGCTCGCCT 11018

RESULT 7
US-08-457-342-6
: Sequence 6, Application US/08457342
: Patent No. 5662898
: GENERAL INFORMATION:
: APPLICANT: Schupp, Thomas
: APPLICANT: Ligon, James M.
: APPLICANT: Beck, James Joseph
: APPLICANT: Hill, Dwight Steven
: APPLICANT: Ryals, John Andrew
: APPLICANT: Gaffney, Thomas Deane
: APPLICANT: Lam, Stephen Ting
: APPLICANT: Hammer, Phillip E.
: APPLICANT: Uknes, Scott Joseph
: TITLE OF INVENTION: Genes for the synthesis of
: TITLE OF INVENTION: antipathogenic substances
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Ciba-Geigy Corporation
: STREET: 7 Skyline Drive
: CITY: Hawthorne
: STATE: NY
: COUNTRY: USA
: ZIP: 10532
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25

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:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/457,342
: FILING DATE: 01-JUN-1995
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/457,205
: FILING DATE: 01-JUN-1995
: APPLICATION NUMBER: 08/258,261
: FILING DATE: 08-JUN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Elmer, James Scott
: REGISTRATION NUMBER: 36,129
: REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-8614
: TELEFAX: 919-541-8689
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 28958 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
:
: US-08-457-342-6
:
:
:
: Alignment Scores:
: Pred. No.: 106 Length: 28958
: Score: 92.50 Matches: 34
: Percent Similarity: 41.28% Conservative: 11
: Best Local Similarity: 31.19% Mismatches: 52
: Query Match: 11.62% Indels: 12
: DB: 1 Gaps: 4
:
: US-09-809-545a-2_COPY_1_148 (1-148) x US-08-457-342-6 (1-28958)
:
: QY 47 SerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAla 66
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 10706 AGCGGCTCCCTCGAGAGGCGGCGGCTTCCTCCGCGAGGCGAGCGCCCATCCGCTGTCA 10765
:
: QY 67 ThrAlaAlaAlaAlaTyr---ArgGlyAlaHis-LeuArgGlyArgGlyArgGlyArgGly 85
:   ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 10766 CGCTCGCCCTCGAGACCTGCGAGCGCTGACCGGCTGATCCCGCTGCTGCGGCTCCA 10825
:
: QY 85 rAsnThrPheArgAlaAlaAlaLapProProProlleProAlaTyrGlyGlyValValTyr 105
:   ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 10826 TTCGAGC--AGAGAGAGGCGCCACCTGCGCGCTGCTCTCTGCGGCGAGCTCTCTA 10882
:
:   105 rGlnGluProValTyrGlyAsnLysLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAl 125
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 10883 CCGGAGGCGCT-----CGCGCTGACTGGAAGACTCTTCGCGCCCTACCGCTCCCC 10933
:
: QY 125 agln-----ProThrProAlaThrAlaAlaAlaTyrSerAspSerTyr 139
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 10934 GCAAGGTCTCTCCCTCCACCTTACCCCTTCACGAGAGCGGTTCTGCTGACGCTCTCA 10993
:
: QY 139 rGlyArgValTyrAlaAlaAlaAspPro 147
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 10994 GGGACGACGCTTCCGACGCTGCGCT 11018
:
: RESULT 8
: US-08-457-646a-6
: Sequence 6, Application US/08457646a
: Patent No. 5679560
:
: GENERAL INFORMATION:
: APPLICANT: Schupp, Thomas
: APPLICANT: Ligon, James M.
: APPLICANT: Beck, James Joseph
: APPLICANT: Hill, Dwight Steven
: APPLICANT: Ryals, John Andrew
: APPLICANT: Gaffney, Thomas Deane
: APPLICANT: Lam, Stephen Ting

```

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:
: APPLICANT: Hammer, Phillip E.
: APPLICANT: Unes, Scott Joseph
: TITLE OF INVENTION: Genes for the synthesis of
: TITLE OF INVENTION: antipathogenic substances
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Ciba-Geigy Corporation
: STREET: 7 Skyline Drive
: CITY: Hawthorne
: STATE: NY
: COUNTRY: USA
: ZIP: 10532
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/457,646A
: FILING DATE: 01-JUN-1995
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/457,205
: FILING DATE: 01-JUN-1995
: APPLICATION NUMBER: 08/258,261
: FILING DATE: 08-JUN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Elmer, James Scott
: REGISTRATION NUMBER: 36,129
: REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-8614
: TELEFAX: 919-541-8689
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 28958 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
:
: US-08-457-646a-6
:
:
:
: Alignment Scores:
: Pred. No.: 106 Length: 28958
: Score: 92.50 Matches: 34
: Percent Similarity: 41.28% Conservative: 11
: Best Local Similarity: 31.19% Mismatches: 52
: Query Match: 11.62% Indels: 12
: DB: 1 Gaps: 4
:
: US-09-809-545a-2_COPY_1_148 (1-148) x US-08-457-646a-6 (1-28958)
:
: QY 47 SerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAla 66
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 10706 AGCGGCTCCCTCGAGAGGCGGCGGCTTCCTCCGCGAGGCGAGCGCCCATCCGCTGTCA 10765
:
: QY 67 ThrAlaAlaAlaAlaTyr---ArgGlyAlaHis-LeuArgGlyArgGlyArgGlyArgGly 85
:   ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 10766 CGCTCGCCCTCGAGACCTGCGAGCGCTGACCGGCTGATCCCGCTGCTGCGGCTCCA 10825
:
: QY 85 rAsnThrPheArgAlaAlaAlaLapProProProlleProAlaTyrGlyGlyValValTyr 105
:   ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 10826 TTCGAGC--AGAGAGAGGCGCCACCTGCGCGCTGCTCTCTGCGGCGAGCTCTCTA 10882
:
:   105 rGlnGluProValTyrGlyAsnLysLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAl 125
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 10883 CCGGAGGCGCT-----CGCGCTGACTGGAAGACTCTTCGCGCCCTACCGCTCCCC 10933
:
: QY 125 agln-----ProThrProAlaThrAlaAlaAlaTyrSerAspSerTyr 139
:   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
: Db 10934 GCAAGGTCTCTCCCTCCACCTTACCCCTTCACGAGAGCGGTTCTGCTGACGCTCTCA 10993

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IMMEDIATE SOURCE:
CLONE: p98/1
US-08-764-233A-4

Alignment Scores:
Pred. No.: 106 Length: 28958
Score: 92.50 Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 11.62% Indels: 12
DB: 1 Gaps: 4

US-09-809-545a-2_COPY_1_148 (1-148) x US-08-764-233A-4 (1-23958)

QY 47 SerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAla 66
Db 10706 AGCGGCTCTCGAGAGATGGGCATCGCTTCGTCGAGGTGACGCCCTCCACCTGCTCA 10765
QY 67 ThrAlaAlaAlaTyr---ArgGlyAlaHis-LeuArgGlyArgGlyArgThrValTy 85
Db 10766 CGCTCGCCCTCCGCGAGACCTCGGAGGCGCTCACCGCTGATCCCGTGTGCTGCGCTCA 10825
QY 85 rAsnThrPheArgAlaAlaAlaProProProIleProAlaTyrGlyGlyValValTy 105
Db 10826 TTCGACG---AGAGAAGAGCCACCTCGCCGCTGCTCTCTCTGCGGCGAGCTCTCA 10882
QY 105 rGlnGluProValTyrGlyAsnLysLeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAl 125
Db 10883 CCGGAGGCT-----CGCGCTCGACTGGAGAGACTTCTTGGCCCTACGCTCCCC 10933
QY 125 agln-----ProThrProAlaThrAlaAlaAlaTyrSerAspSerTy 139
Db 10934 GCAAGTCTCCCTCCACCACTACCCCTTCCAGCGAGAGCGGTCTGCTGCACTCTCA 10993
QY 139 rGlyArgValTyrAlaAlaAspPro 147
Db 10994 CGGAGCAACGCTTCCGACGTGCCT 11018

RESULT 11
US-08-457-335A-6
Sequence 6, Application US/08457335A
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESS: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,335A
FILING DATE: 01-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205

FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-457-335A-6

Alignment Scores:
Pred. No.: 106 Length: 28958
Score: 92.50 Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 11.62% Indels: 12
DB: 1 Gaps: 4

US-09-809-545a-2_COPY_1_148 (1-148) x US-08-457-335A-6 (1-28958)

QY 47 SerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAla 66
Db 10706 AGCGGCTCTCGAGATGGGCATCGCTTCGTCGAGGTGACGCCCTCCACCTGCTCA 10765
QY 67 ThrAlaAlaAlaTyr---ArgGlyAlaHis-LeuArgGlyArgGlyArgThrValTy 85
Db 10766 CGCTCGCCCTCCGCGAGACCTCGGAGGCGCTCACCGCTGATCCCGTGTGCTGCGCTCA 10825
QY 85 rAsnThrPheArgAlaAlaAlaProProProIleProAlaTyrGlyGlyValValTy 105
Db 10826 TTCGACG---AGAGAAGAGCCACCTCGCCGCTGCTCTCTCTGCGGCGAGCTCTCA 10882
QY 105 rGlnGluProValTyrGlyAsnLysLeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAl 125
Db 10883 CCGGAGGCT-----CGCGCTCGACTGGAGAGACTTCTTGGCCCTACGCTCCCC 10933
QY 125 agln-----ProThrProAlaThrAlaAlaAlaTyrSerAspSerTy 139
Db 10934 GCAAGTCTCCCTCCACCACTACCCCTTCCAGCGAGAGCGGTCTGCTGCACTCTCA 10993
QY 139 rGlyArgValTyrAlaAlaAspPro 147
Db 10994 CGGAGCAACGCTTCCGACGTGCCT 11018

RESULT 12
US-08-729-214-6
Sequence 6, Application US/08729214
Patent No. 5817502
GENERAL INFORMATION:
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Hammer, Phillip E.
APPLICANT: van Pee, Karl-Heinz
APPLICANT: Kirner, Sabine
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESS: Ciba-Geigy Corporation
STREET: 520 White Plains Road
CITY: Tarrytown

STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25*
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,214
FILING DATE: TBA
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1506/CIP5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-729-214-6

Alignment Scores:
Pred. No.: 106 Length: 28958
Score: 92.50 Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 11.62% Indels: 12
DB: 1 Gaps: 4

US-09-809-545a-2_COPY_1_148 (1-148) x US-08-729-214-6 (1-28958)
QY 47 SerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaIa 66
DB 10706 ACCGCTCTCTCGACATGGGCAATCGCTTCTCCGTGAGGTGAGCCCAATCCGCTCTCA 10765
QY 67 ThrAlaAlaAlaTyr---ArgGlyAlaHis-LeuArgGlyArgGlyValTyr 85
DB 10766 CGCTCGCCCTCGCGAGACCTCGAGCGCTCACCGCTGATCCCGCTGCTGCGCTCA 10825
QY 85 rAsnThrPheArGAlaAlaAlaProProProProleProAlaTyrGlyGlyValValTyr 105
DB 10826 TTCGACG---AGAAAGAGCCACCTCGCCGCTCTCTCTCGCGGCGGAGCTCTCTA 10882
QY 105 rGlnGluProValTyrGlyAsnLysLeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAl 125
DB 10883 CCGGAGGCT-----CGGCTCGACTGGAAGACTTGTCCGCGCTACGCTCCCC 10933
QY 125 agln-----ProThrProAlaThrAlaAlaTyrSerAspSerTyr 139
DB 10934 GCAAGGTCTCCCTCCCACTACCTACCTCCAGAGAGGCGTTCGGCTCGACGCTCA 10993
QY 139 rGlyArgValTyrAlaAlaAspPro 147
DB 10994 CGGACGAACGCTTCGAGCTCGCT 11018

RESULT 13
US-09-028-934-6
Sequence 6, Application US/09028934
Patent No. 6117670
GENERAL INFORMATION:
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight S.
APPLICANT: Lam, Steven T.
APPLICANT: Hammer, Phillip E.

APPLICANT: van Pee, Karl-Heinz
APPLICANT: Kliner, Sabine
APPLICANT: Young, Thomas R.
TITLE OF INVENTION: Pyrolytic Biosynthesis Genes and Uses
TITLE OF INVENTION: thereof
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: No. 6117670artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,934
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/729,214
FILING DATE: 09-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,261
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1506/CIP7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-028-934-6

Alignment Scores:
Pred. No.: 106 Length: 28958
Score: 92.50 Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 11.62% Indels: 12
DB: 3 Gaps: 4

US-09-809-545a-2_COPY_1_148 (1-148) x US-09-028-934-6 (1-28958)
QY 47 SerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaIa 66
DB 10706 ACCGCTCTCTCGACATGGGCAATCGCTTCTCCGTGAGGTGAGCCCAATCCGCTCTCA 10765
QY 67 ThrAlaAlaAlaTyr---ArgGlyAlaHis-LeuArgGlyArgGlyValTyr 85
DB 10766 CGCTCGCCCTCGCGAGACCTCGAGCGCTCACCGCTGATCCCGCTGCTGCGCTCA 10825
QY 85 rAsnThrPheArGAlaAlaAlaProProProProleProAlaTyrGlyGlyValValTyr 105
DB 10826 TTCGACG---AGAAAGAGCCACCTCGCCGCTCTCTCTCGCGGCGGAGCTCTCTA 10882
QY 105 rGlnGluProValTyrGlyAsnLysLeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAl 125
DB 10883 CCGGAGGCT-----CGGCTCGACTGGAAGACTTGTCCGCGCTACGCTCCCC 10933
QY 125 agln-----ProThrProAlaThrAlaAlaTyrSerAspSerTyr 139

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Db      10934 GCAAGGTCTCCTCCACCTACCCCTTCAGAGAGCGTTGTGCTGACGTCTCCA 10993
QY      139 rglaryvaltyralalalspro 147
Db      10994 CGAGCAGAACGCTTCGACGTCCGCT 11018

RESULT 14
US-08-764-233A-1
; Sequence 1, Application US/08764233A
; Patent No. 571849
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Schupp, Thomas
; APPLICANT: Beck, James J.
; APPLICANT: Hill, Dwight S.
; APPLICANT: Neff, Snezana
; APPLICANT: Ryals, John A.
; TITLE OF INVENTION: Genes for The Biosynthesis Of Soraphen
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,233A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/729,214
; FILING DATE: 09-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/258,261
; FILING DATE: 08-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: 1506/CIP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49377 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Sorangium cellulosum
; IMMEDIATE SOURCE:
; CLONE: p98/1, pL3, and pVKM15
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 383..760
; OTHER INFORMATION: /product= "Sora"
; OTHER INFORMATION: /note= "This gene encodes a protein that is highly homologous
; OTHER INFORMATION: the reductase domains of type I PKSs such as eryA from
; OTHER INFORMATION: Saccharopolyspora erythraea."
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 927..19874
; OTHER INFORMATION: /product= "Sora"
; OTHER INFORMATION: /note= "Gene product is highly homologous to type I PKSs that
; OTHER INFORMATION: are known to be involved in the synthesis of polyketide

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; OTHER INFORMATION: compounds."
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 942..7115
; OTHER INFORMATION: /product= "Module 1 of Sora"
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 7203..12884
; OTHER INFORMATION: /product= "Module 2 of Sora"
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 13455..19616
; OTHER INFORMATION: /product= "Module 3 of Sora"
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 19871..46318
; OTHER INFORMATION: /product= "Sorb"
; OTHER INFORMATION: /note= "Gene product is highly homologous to type I PKSs
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 19870..24556
; OTHER INFORMATION: /product= "Module 1 of SorB"
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 24638..30820
; OTHER INFORMATION: /product= "Module 2 of SorB"
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 30881..35446
; OTHER INFORMATION: /product= "Module 3 of SorB"
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 35528..40114
; OTHER INFORMATION: /product= "Module 4 of SorB"
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 40190..46318
; OTHER INFORMATION: /product= "Module 5 of SorB"
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 46851..47891
; OTHER INFORMATION: /product= "Sorm"
; OTHER INFORMATION: /note= "The protein encoded by the sorm gene is highly
; OTHER INFORMATION: homologous to the methyltransferase from Streptomyces
; OTHER INFORMATION: hygroscopicus that is involved in the synthesis of the
; OTHER INFORMATION: polyketide rapamycin."
; US-08-764-233A-1

Alignment Scores:
Pred. No.: 214 Length: 49377
Score: 92.50 Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 11.62% Indels: 12
DB: 1 Gaps: 4

US-09-809-545a-2_copy_1_148 (1-148) x US-08-764-233A-1 (1-49377)
QY 47 SerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAla 66
Db 27009 AGCGGCTCCCTGACATGGCATGCGCTTCCTCGAGGACGACCCCGCTGCTCA 27068
QY 67 ThrAlaAlaAlaAlaTyr---ArgGlyAlaHis-LeuArgGlyArgGlyArgThrValTy 85
Db 27069 CGCTCCCGCTCCGCGAGACCTGCGACCGCTCGATCCCGTGTGCTGCGCTCCA 27128
QY 85 rAsnThrPheArgAlaAlaAlaProProPheProAlaProAlaTyrGlyGlyValValTy 105
Db 27129 TTGAGAG---AGAAGAAGGACACCTGCGCGCTGCTCTCTGCGGAGGAGCTGTCA 27185
QY 105 rGlnGluProValTyrGlyAsnLysLeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAl 125
Db 27186 CCGGAGGCGCT-----CGCGCTGACGTGGAAGGACATTCTCGGCGCTTACGCTCC 27236

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QY 125 acIn-----ProThrProAlaThrAlaAlaAlaTyrSerAspSerTy 139
DB 27237 GCAAGCTCTCCCTCCCACTACCCCTTCACGAGCGGTTGCGTCGACGCTCCA 27296
QY 139 rGlyArgValTyrAlaAlaAspPro 147
DB 27297 CGGACGAACGCTTCCGACGTCGCT 27321

RESULT 15
US-08-990-823-62
: Sequence 62, Application US/08990823D
: Patent No. 6228371
: GENERAL INFORMATION:
: APPLICANT: Nano, Francis
: TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
: TITLE OF INVENTION: Immunostimulatory Peptides
: FILE REFERENCE: 49086
: CURRENT APPLICATION NUMBER: US/08/990,823D
: CURRENT FILING DATE: 1997-12-15
: EARLIER APPLICATION NUMBER: US 96/10375
: EARLIER FILING DATE: 1996-06-14
: EARLIER APPLICATION NUMBER: 60/000,254
: EARLIER FILING DATE: 1995-06-15
: NUMBER OF SEQ ID NOS: 113
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 62
: LENGTH: 821
: TYPE: DNA
: ORGANISM: Mycobacterium tuberculosis
: FEATURE:
: NAME/KEY: Modified base
: OTHER INFORMATION: n represents a or g or c or t/u
: US-08-990-823-62

Alignment Scores:
Pred. No.: 1,39 Length: 821
Score: 91.00 Matches: 45
Percent Similarity: 30.85% Conservative: 13
Best Local Similarity: 23.94% Mismatches: 76
Query Match: 11.43% Indels: 54
DB: 3 Gaps: 6

US-09-809-545a-2_COPY_1_148 (1-148) x US-08-990-823-62 (1-821)
QY 1 MethrAsnLysLysAlaValAsnProTyrThrAsnGlyTyrPlyLeuAsnProVal 20
DB 70 ATGGCGGACGACGTCTGCGCGGACGCCAATGCGGATGCTGCAACCGGTTCG 129
QY 21 GlyAlaValTyrSerProAspPheTyrAlaGlyThrValLeuLeuCysGlnAlaAsn 40
DB 130 GGCCAGCGCTTCGACGCGGACGCGTGGCGGTATCATGCCGCTTCAAAACCG 189
QY 41 GluGlySerSerMetTyrSerGlyProSer-----SerLeuValTyr 54
DB 190 AGGCGCTGGCGAGGACCTCAAGTCCGANCAGCGGCTGCTCCAAACCGGCTGTCAAC 249
QY 55 ThrSerAlaMetProGlyPheProTyrProAlaAlaThrAlaAlaAlaTyrArgGly 74
DB 250 TCCGATGCGTGGCCCAACAAACCGCGCATCAGACTCCGCGGCGACCGCGGCA 309
QY 74 ----- 74
DB 310 GGGAAGGCGCGGNTCGGATNCAAGGGTTGCNAGCGCGCTGCCGTCNGATTTGA 369
QY 75 -----AlaHisLeuArgGlyArg-----GlyArgThrValTyr 85
DB 370 CCCGCGACGTACCCCGCGGATGGGAGGAGGAACAACCTGGCGCGCACGCGCAC 429
QY 86 AsnThrPheArgAlaAlaAlaProProProProAlaTyrGlyGlyValValTyr 105
DB 430 CTCGGCCGTGTACAGTACCGCCCGGACCGCGCGCTGTGTGT----- 480

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QY 106 GlnGluProValTyrGlyAsnLys-----LeuLeuGlnGlyGly----- 118
DB 481 -----GGTTTCCGGCGCGCGCCCATCTGTGTCTACAAGAGGAGACGGCATTCATCTA 534
QY 119 -----TyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
DB 535 CGGCGAGTCCCTGAACACTGCAGTGGGGCGTCACGCGCGGACGCGCGCATTCACGCACT 594
QY 132 AlaAlaAlaTyrSerAspSerTyr 139
DB 595 GGGCGCAGTATTTCGATCGACAT 618

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Search completed: September 25, 2003, 12:13:58
Job time : 102 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 25, 2003, 12:07:20 ; Search time 148 Seconds
(without alignments)
2489.491 Million cell updates/sec

Title: US-09-809-545A-2_COPY_1_148
Perfect score: 796
Sequence: 1 MTNKKAVNPYNGMKINPVV.....PATAAASDPSGCVYAADPY 148

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1678620 seqs, 1244745471 residues
Total number of hits satisfying chosen parameters: 3357240

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame_plus_p2n.model -DEV=tlp
-Q=/cgn2_1/USPTO.spool.p/US09809545/rnatc_25092003_111136_23219/app_query.fasta-1.327
-DB=Published_Applications_NA -QFMT=fastlap -SUFFIX=rmpb -MIMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blissum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100
-THR.MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09809545 @cgn_1.1.85 @rnatc_25092003_111136_23219
-NCPU=6 -ICPU=3 -NO.MAP -LARGEQUERY -NRG.SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THEADS=1 -XGAPOP=10 -XGAPEXT=0.5
-Fgapop=6 -Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------------------------|
| 1 | 796 | 100.0 | 1340 | 10 | US-09-809-545A-1 Sequence 1, Appl1 |

| | | | | | |
|----|-------|------|---------|----|---------------------|
| 2 | 674 | 84.7 | 2372 | 9 | US-09-794-591-1 |
| 3 | 441.5 | 55.5 | 1843 | 11 | US-09-919-039-266 |
| 4 | 379 | 47.6 | 1506 | 12 | US-10-359-385-5 |
| 5 | 94 | 11.8 | 657 | 10 | US-09-974-300-1655 |
| 6 | 92.5 | 11.6 | 699 | 13 | US-10-027-632-24830 |
| 7 | 92.5 | 11.6 | 699 | 13 | US-10-027-632-24831 |
| 8 | 92.5 | 11.6 | 699 | 13 | US-10-027-632-24832 |
| 9 | 92.5 | 11.6 | 11447 | 12 | US-10-027-632-24833 |
| 10 | 92.5 | 11.6 | 11447 | 12 | US-10-027-632-24834 |
| 11 | 92.5 | 11.6 | 11447 | 12 | US-10-027-632-24835 |
| 12 | 92.5 | 11.6 | 11447 | 12 | US-10-027-632-24836 |
| 13 | 91 | 11.4 | 821 | 11 | US-10-177-293-60 |
| 14 | 91 | 11.4 | 821 | 11 | US-10-177-293-61 |
| 15 | 91 | 11.4 | 821 | 11 | US-10-177-293-62 |
| 16 | 90 | 11.3 | 466 | 11 | US-10-198-846-11039 |
| 17 | 89.5 | 11.2 | 3285 | 10 | US-09-996-634-62 |
| 18 | 89 | 11.2 | 3285 | 10 | US-09-997-182-62 |
| 19 | 87.5 | 11.0 | 2658 | 9 | US-09-997-181-62 |
| 20 | 87.5 | 11.0 | 2658 | 9 | US-09-998-995-8998 |
| 21 | 87.5 | 11.0 | 3231 | 8 | US-09-712-353-143 |
| 22 | 87.5 | 11.0 | 4182 | 12 | US-10-156-761-1 |
| 23 | 87.5 | 11.0 | 10278 | 12 | US-10-156-761-1 |
| 24 | 86 | 10.8 | 1963 | 12 | US-08-815-242-4035 |
| 25 | 86 | 10.8 | 2179 | 13 | US-08-814-353-20319 |
| 26 | 85.5 | 10.7 | 2208 | 14 | US-09-820-788-3 |
| 27 | 85 | 10.7 | 1383 | 14 | US-10-205-219-182 |
| 28 | 85 | 10.7 | 1743 | 10 | US-10-027-632-97742 |
| 29 | 85 | 10.7 | 6930 | 13 | US-10-037-270-502 |
| 30 | 85 | 10.7 | 53522 | 11 | US-10-156-761-1 |
| 31 | 85 | 10.7 | 9025608 | 14 | US-09-904-968A-1 |
| 32 | 84.5 | 10.6 | 969 | 14 | US-10-125-635A-452 |
| 33 | 84.5 | 10.6 | 1494 | 14 | US-10-104-693-1 |
| 34 | 84.5 | 10.6 | 1497 | 9 | US-08-322-678-6 |
| 35 | 84.5 | 10.6 | 1497 | 9 | US-09-060-854B-1 |
| 36 | 84.5 | 10.6 | 1497 | 14 | US-10-033-335-1 |
| 37 | 84.5 | 10.6 | 1497 | 14 | US-10-228-572-1 |
| 38 | 84.5 | 10.6 | 4244 | 11 | US-09-760-285-27 |
| 39 | 84.5 | 10.6 | 4244 | 11 | US-09-760-285-27 |
| 40 | 84.5 | 10.6 | 4244 | 11 | US-10-240-965-250 |
| 41 | 84.5 | 10.6 | 4264 | 11 | US-09-912-697-15 |
| 42 | 84.5 | 10.6 | 4264 | 12 | US-10-270-839-36 |
| 43 | 84.5 | 10.6 | 4264 | 12 | US-10-371-634-16 |
| 44 | 84.5 | 10.6 | 4264 | 12 | US-10-348-074-1 |
| 45 | 84.5 | 10.6 | 62944 | 10 | US-10-171-581-28 |

ALIGNMENTS

RESULT 1
US-09-809-545A-1
; Sequence 1, Application US/09809545A
; Patent No. US20020110804A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, Lawrence W.
; APPLICANT: White, R. Tyler
; TITLE OF INVENTION: SECRETED FACTORS
; FILE REFERENCE: SCIOS 017A
; CURRENT APPLICATION NUMBER: US/09/809,545A
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1340
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-09-809-545A-1

Alignment Scores:

| | | | |
|------------------------|----------|---------------|------|
| Pred. No.: | 4.64e-85 | Length: | 1340 |
| Score: | 796.00 | Matches: | 148 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |

DB: 10 Gaps: 0

US-09-809-545a-2_COPY_1_148 (1-148) x US-09-809-545a-1 (1-1340)

OY 1 MethrasnlyslsAlaValAsnProtyrThrAsnGlyTblyslsLeuAsnProValaVal 20
|||||
DB 535 ATGACTAATAAAGGCGGTGACACCCCTACACCAATGGCTGGAAATTAAATCCAGTTGTG 594
21 GAlaValaValTyrSerProAspPheTyrAlaGlyThrValaLeuLeuCySGlnAlaAsnGln 40
|||||
DB 595 GGCGGCGCTACAGCCCGGACCTTCATGTCAGGACGCGTGTGTGTCAGGACGACAG 654
OY 41 GluGlySerSerMetTyrSerGlyProSerSerLeuValTyrThrSerAlaMetProGly 60
|||||
DB 655 GAGGAGTCTTCACATGTCAGAGCGCCCGCTTGTATATCTTGTGCAATGCTGTGC 714
OY 61 PheProTyrProAlaAlaThrAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 80
|||||
DB 715 TTTCATATCCGCGCGCCGACCTGCTGACCTGATACAGAGGCGCTCACCTTCAGAGCGCT 774
OY 81 GAlaTgThrValaTyrAsnThrPheAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 100
|||||
DB 775 GGTGCGACCGGTGTCACACACCTTCAGAGCTGCGGCGCCCGACCCCAATCCCGGCTAT 834
OY 101 GlyGlyValaValTyrGlnGluProValaTyrGlyAsnLysLeuGlnGlyGlyTyrAla 120
|||||
DB 835 GCGGAGTAGTGTATCAAGACGACGATGATGCAATTAATTCCTACAGGGGTGTACCT 894
OY 121 AAlaTgTgTyrAlaGlnProThrProAlaThrAlaAlaAlaTyrSerAspSerTyrGly 140
|||||
DB 895 GCATACCGCTACGCCACCCACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 954
OY 141 ArgValaTyrAlaAlaAspProTyr 148
|||||
DB 955 CGAGTTTATGCTGCCGACCCCTAC 978

RESULT 2

US-09-794-591-1

Sequence 1, Application US/09794591

Patent No. US20010018198A1

GENERAL INFORMATION:

APPLICANT: Pulist, Stefan M.

APPLICANT: Shibata, Hiroki

TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,

TITLE OF INVENTION: Products Related Thereto and Methods of Using Same

FILE REFERENCE: CE 3093

CURRENT APPLICATION NUMBER: US/09/794,591

PRIOR FILING DATE: 2001-02-26

PRIOR APPLICATION NUMBER: 09/145,391

PRIOR FILING DATE: 1998-09-01

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 2372

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (987)..(1979)

US-09-794-591-1

Alignment Scores:

Pred. No.: 2,92e-70 Length: 2372

Score: 674.00 Matches: 136

Percent Similarity: 83.23% Conservative: 3

Best Local Similarity: 81.44% Mismatches: 8

Query Match: 84.67% Indels: 2

DB: 9 Gaps: 2

US-09-809-545a-2_COPY_1_148 (1-148) x US-09-794-591-1 (1-2372)

OY 1 MethrasnlyslsAlaValAsnProtyrThrAsnGlyTblyslsLeuAsnProValaVal 20
|||||
|||||

DB 1572 ATGACAAATAAAGACCGCTACACCTTATACAAATGGCTGGAAATTCAGTTGTG 1631

OY 21 GAlaValaValTyrSerProAspPheTyrAlaGlyThrValaLeuLeuCySGlnAlaAsnGln 40
|||||

DB 1632 GGTGCGACCGGTGTCACACCTTCATGTCAGGACGCGTGTGTGTCAGGACGACAG 1691

OY 41 GluGlySerSerMetTyrSerGlyProSerSerLeuValTyrThrSerAlaMetProGly 60
|||||

DB 1692 GAGGAGTCTTCACATGTCAGAGCGCCCGCTTGTATATCTTGTGCAATGCTGAGGC 1751

OY 61 PheProTyrProAlaAlaThrAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 80
|||||

DB 1752 TTCCCGTATCCAGACGACCGCCGCGGCGCTTACAGAGGCGGACCTGCGAGGCGG 1811

OY 81 GAlaTgTgTyrAlaGlnProThrPheAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 100
|||||

DB 1812 GGTGCGACCGGTGTCACACCTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTAC 1871

OY 101 GlyGlyValaValTyrGlnGluProValaTyrGlyAsnLysLeuGlnGlyGlyTyrAla 120
|||||

DB 1872 GCGCGTGTGTATCCCGAGATGATTTATGTCAGAGC---ATTATGCTGTATATGC 1928

OY 120 AAlaTgTgTyrAlaGlnProThrProAlaThrAlaAlaAlaAlaTyrSerAspSer----- 138

DB 1929 TGCATACCGCTACCGCCGACCTTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1987

OY 139 -----TyrGlyArgVa 142
|||||

DB 1988 AGTTCGCTGCTGTGACAGACAGATGAATTTCTGTACACCTTCGAGTTACGAGCAGT 2047

OY 142 ITyrAlaAlaAspProTyr 148
|||||

DB 2048 TTATGCTGCGACCCCTAC 2066

RESULT 3

US-09-919-039-266

Sequence 266, Application US/09919039

Publication No. US20030108871A1

GENERAL INFORMATION:

APPLICANT: Kaser, Matthew R.

TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES

FILE REFERENCE: PA-0035 US

CURRENT APPLICATION NUMBER: US/09/919,039

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: 60/222,113

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 401

SOFTWARE: PERL Program

SEQ ID NO 266

LENGTH: 1843

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc.feature

OTHER INFORMATION: Incyte ID No. US20030108871A1 253763.3

US-09-919-039-266

Alignment Scores:

Pred. No.: 8,93e-43 Length: 1843

Score: 441.50 Matches: 96

Percent Similarity: 51.02% Conservative: 4

Best Local Similarity: 48.98% Mismatches: 19

Query Match: 55.46% Indels: 77

DB: 11 Gaps: 5

US-09-809-545a-2_COPY_1_148 (1-148) x US-09-919-039-266 (1-1843)

OY 1 MethrasnlyslsAlaValAsnProtyrThrAsnGlyTblyslsLeuAsnProValaVal 20
|||||
|||||

| | | | |
|----|------|---|------|
| Db | 1228 | ATGACCAACAAAGAAGACGGGGAACCCCTACACCAAGCGCTGGAAGCTAAATCCAGTGTCT | 1287 |
| Qy | 21 | GIYAlaValaIYrSerProAsPheTyraIaGlyThraValLeuLeuCysGlnAlaasnGln | 40 |
| Db | 1288 | GGCCGACGCTACGGGGCCCTGAATCTCATGCACTGACG | 1323 |
| Qy | 41 | GIuGlySerSerMetTYrSerGlyProSerSerLeuValTYrThrSerAlaMetProGly | 60 |
| Db | 1324 | -----GGG | 1326 |
| Qy | 61 | PheProTYrProAlaAlaThraAlaAlaAlaIaTYrArgGlyAlaHisLeuArgIYarg | 80 |
| Db | 1327 | TTCCCTTACCCACCACCCAGCCGTCGCTTACCGGGGCGACATCTTCGGGGCCGG | 1386 |
| Qy | 81 | GIYArgThraValTYrAsnThrPheArgAlaAlaIaProProProProIleProAlaTYr | 100 |
| Db | 1387 | GGCGGGGCGCGTAAATATACATTTCGGGCTCGCGACCCACCCCATCCGACCTTAC | 1446 |
| Qy | 101 | GIYgLy----- | 102 |
| Db | 1447 | GGAGCGGCACTGAGACAACCGTTGTTAAAAATGCCAGTCCATGAGCGGGCTGGACCG | 1506 |
| Qy | 102 | ----- | 102 |
| Db | 1507 | TGCCCCCTCCTCCTCAGACAGACACCGAGCCGGCCTACCCCACTCTCCAGCGTTCCCA | 1566 |
| Qy | 103 | -----ValaValTYrGlnGluProValaTYrGlyAsnIys | 113 |
| Db | 1567 | CCACTTTCCTTCGCGTTGCTTCACAGGCTGCTGATACAGATGGATTTTATATGCTGTGAG | 1626 |
| Qy | 114 | LeuLeuGlnGlyGlyTYrAlaAlaIaTYrArgTYrAlaGlnProThrProAlaThraAla | 133 |
| Db | 1627 | ---ATTATATGAGGCTACGACGCTACAGATACCTCAGCCCGCT---GCAGCGGGCGCA | 1680 |
| Qy | 134 | AlaTYrSerAspSerTYrGlyArgValTYr---AlaAlaAspProTYr | 148 |
| Db | 1681 | GCTTACACCGACAGTTTAGCGAGAGTCTACCACTGCGACCGCTAC | 1728 |

```

RESULT 4
US-10-359-385-5
Sequence 5, Application US/10359385
Publication NO. US20030143622A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Lu, Alma
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
FILE REFERENCE: PF-0611 US
CURRENT APPLICATION NUMBER: US/10/359,385
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/176,657
PRIOR FILING DATE: 1998-10-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PERL Program
SEQ ID NO 5
LENGTH: 1506
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: _
OTHER INFORMATION: 1250374
US-10-359-385-5

```

Alignment Scores:

| | | | |
|------------------------|----------|---------------|------|
| Pred. No.: | 1,856=35 | Length: | 1506 |
| Score: | 379.00 | Matches: | 86 |
| Percent Similarity: | 59.63% | Conservative: | 10 |
| Best Local Similarity: | 53.44% | Mismatches: | 37 |
| Query Match: | 47.61% | Indels: | 29 |
| DB: | 12 | Gaps: | 6 |

```

US-09-809-545A-2_COPY_1_148 (1-148) x US-10-359-385-5 (1-1506)
OY 1 MethrAsnLysLysAlaValAsnProTyrThrAsnGlyTyrPLeuAsnProValVal 20
Db ATGACCATAGAGAGATGAGTGCACACCATATGCAAATGTTGGAAATTAAAGCCAGTACT 827
OY 21 GAlaValAlaTyrSerProAspPheTyrTrlaGlyThrValLeuLeuCysGlnAlaAsn--- 39
Db GGACCTGATATATGGTCCGAGCTTATATGACACCATCCACCTTTCAAAGCAGATGTGTCCCTA 887
OY 40 --GlnGluGlySerSerMetTyrSerGlyProSerSerLeu-----ValTyrThrSer 56
Db 888 GGCATATGTCAGCAGCAGTCCCTCTATCAGGAAGAGGGGCTATCACACTTACATTCCTTTTA 947
OY 57 AlaMetProGlyPheProTyrPro---AlaAlaThrAlaAlaAlaAlaTyrArgGlyAla 75
Db ATCATTTCTGGCTTCCCTTACCTACAGTCAGCACACACGACGCGCGCTTTCAGAGAGACC 1007
OY 76 HisLeuArgGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaAlaProProPro 95
Db 1008 CATTTGAGGGCGACAGGGCGACGATATATGTCGACGCCA---GCGGTACTCTCAACA 1064
OY 96 ProLeuProAlaTyrGlyGlyValValTyrGlnGluProValTyrGlyAsnLysLeuLeu 115
Db 1065 GCCATTCCTCCCGGCTTACC----- 1081
OY 116 GlnGlyGlyTyrTrlaAlaTyrArgTyrAlaGlnProThrProAlaThr----- 131
Db 1082 AGGGGTGATATGACAGCTTACAGATATGACACAGCTGCTACTGCACCGCAGCCAGCGCT 1144
OY 132 -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyrTrlaAlaAspPro 147
Db 1142 GCTGCAGCGCGTGCAGCGCTTACAGTACGCGTATGCGAGGAGGTACACAGCCGACGCC 1201
OY 148 Tyr 148
Db 1202 TAC 1204

```

```

RESULT 5
US-09-974-300-1655
; Sequence 1655, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berk, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085,500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/6680,558
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1655
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(657)
; OTHER INFORMATION: n = A,T,C or G
US-09-974-300-1655

```

Alignment Scores:

| | | | |
|------------------------|--------|---------------|-----|
| Pred. No.: | 0.0478 | Length: | 657 |
| Score: | 94.00 | Matches: | 38 |
| Percent Similarity: | 40.15% | Conservative: | 17 |
| Best Local Similarity: | 27.74% | Mismatches: | 58 |
| Query Match: | 11.81% | Indels: | 24 |
| DB: | 10 | Gaps: | 8 |

[illegible][illegible]

```

RESULT 7
US-10-027-632-24831
; Sequence 24831, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24831
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-24831

Alignment Scores:
Pred. No.: 0.0778
Score: 92.50
Percent Similarity: 37.76%
Best Local Similarity: 28.67%
Query Match: 11.62%

DB: 13
Gaps: 6
Length: 699
Matches: 41
Conservative: 13
Mismatches: 41
Indels: 48

```

```

OY      25 SerProaspherethylaglythrValLeuleucysglnAla-AsngIngluglyserse 44
Db      84 ACACACGACAGAACGGGGGTCAATTCCTCTGTCTGTGGCTCA-----YTGg 134
OY      44 rMethylSerglyProSerSerleuValIythrSerAlaMetProGlyPheProTyrr- 63
Db      135 ACAAGTCTCAGGCCCCAGGCATCTC---CAGSMACCCAGGGCGTGGCTGTCTTACCA 191
OY      64 -----ProAlaAlaThrAlaAlaAlaTyragl 74
Db      192 CTGACCTACCAAGTCCCTCCCAAGTGCACGCTCCACCTCTCTCCCTTGCCACAGG 251
OY      74 yAlaHisLeuArgLyArg----- 80
Db      252 AGAARACCTAAATTCGAATTCCTCAACGCGATAGAGAGTACAGATCTTGCGCTCC 311
OY      81 -----GlyArgThrValIythrAsnThrPheargAlaAlaAlaProPro 95
Db      312 TGGTGGCCCTGCACCGGGGCACACCTCTCCACGACATGTCGTGAsnATGCTCCCTCC 371
OY      95 oProIleProAlaTyrglyGlyVal-----Val-TyrgIngluProAlaTyrglyAla 112
Db      372 TCCAGGCGCTTCTTACAGTGGGGGTCTCTCGGAATCTCTTCCCAACCCATCTACGCCAA 431
OY      112 sulys-LeuLeuIngluInglyTyrgAlaAlaTyragTyrgAlaIngluProThrAlaThr 131
Db      432 ATCTGCTCTTCCGAGCG-----CCAGTCCAGGCCCG 466
OY      132 Ala 132
Db      465 GCA 467

```

```

RESULT 8
US-10-027-632-24832
Sequence 24832, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
CURRENT FILING DATE: 2002-04-30
PRIORITY APPLICATION NUMBER: US 60/218,006
PRIORITY FILING DATE: 2000-07-12
PRIORITY APPLICATION NUMBER: US 60/198,676
PRIORITY FILING DATE: 2000-04-20
PRIORITY APPLICATION NUMBER: US 60/193,483
PRIORITY FILING DATE: 2000-03-29
PRIORITY APPLICATION NUMBER: US 60/185,218
PRIORITY FILING DATE: 2000-02-24
PRIORITY APPLICATION NUMBER: US 60/167,363
PRIORITY FILING DATE: 1999-11-23
PRIORITY APPLICATION NUMBER: US 60/156,358
PRIORITY FILING DATE: 1999-09-28
PRIORITY APPLICATION NUMBER: US 60/146,002
PRIORITY FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24832
LENGTH: 699
TYPE: DNA
ORGANISM: Human
US-10-027-632-24832

```

Alignment Scores:

Pred. No.:

Score:

Percent Similarity

Best Local Similarity

Query Match:

DB:

```

Length: 699
Matches: 41
Conservative: 13
Mismatch: 41
Indels: 48
Gaps: 6

```

9

```

US-09-809-545A-2_COPY_1_148 (1-148) x US-10-027-632-24832 (1-699)
Oy 25 SerProAspPheTyrAlaGlyThrValLeuLeucGlyAla-AsnGlnGlnGlySerse 44
Db 84 ACACCAACAGAACAGGGGGCTTCATTCCTCTGCTCTGCTGCTCA-----YCTGG 134
Oy 44 rMeTtySerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyr-- 63
Db 135 ACAAGTCTCAGGGCCCAAGCATCTC---CAGGWAAGACCCAGGGCTGCTGCTTACCA 191
Oy 64 -----ProAlaAlaThrAlaAlaAlaAlaTyrATyG 74
Db 192 CTGACCTCACCAGATCCCTCCCAAGTGCACAGCTCCACCTCTCTCCCTGCCAGAG 251
Oy 74 yAlaHisLeuArgGlyArg----- 80
Db 252 AGAARACCTAAATCGAAATCTCCACAGTGGATGAGAGTACAGAGTCTTGCCCTGCC 311
Oy 81 -----GlyATgThrValTyrAsnThrPheArgAlaAlaAlaProProP 95
Db 312 TGTGCCCCCTGACCCGGGACACCTCTCCACAGACATGTCTGATGTCTCCCTCC 371
Oy 95 oProLLeProAlaTyrGlyGlyVal-----Val-TyrGlnGluProValTyrGly 112
Db 372 TCCAGGGCCCTTCTACAGTGGGGTCTCTGSAATGCTCTTCCCAACCCATCTACGAA 431
Oy 112 snLys-LeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
Db 432 ATCTGCTCTTCCAGGC-----CCCAgTCCAGCCCG 464
Oy 132 Ala 132
Db 465 GCA 467

RESULT 9
US-10-301-822-25
Sequence 25, Application US/10301822
Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MP001-029P2RM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIORITY APPLICATION NUMBER: US 60/339,971
PRIORITY FILING DATE: 2001-12-10
PRIORITY APPLICATION NUMBER: US 60/361,978
PRIORITY FILING DATE: 2002-03-05
PRIORITY APPLICATION NUMBER: US 60/381,988
PRIORITY FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: PastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 11447
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(9192)
US-10-301-822-25

Alignment Scores:
Pred. No.: 2.46 Length: 11447
Score: 92.50 Matches: 28

```

US-10-301-822-25

Alignment Scores:

Pred. No.: 20

Score: 92

```
Length: 11447
Matches: 28
```

14

2

| | |
|-------------------|-----|
| erSe | 44 |
| CTGG | 134 |
| yr-- | 63 |
| | |
| AACCA | 191 |
| rgl | 74 |
| | |
| GAGG | 251 |
| ---- | 80 |
| CTCC | 311 |
| ropr | 95 |
| | |
| CTCC | 371 |
| gl ₁ a | 112 |
| | |
| GCAA | 431 |
| earhr | 131 |
| | |
| CCCG | 464 |

Percent Similarity: 39.22% Conservative: 112
 Best Local Similarity: 27.45% Mismatches: 41
 Query Match: 11.62% Indels: 21
 DB: 12 Gaps: 4

US-09-809-545a-2_COPY_1_148 (1-148) x US-10-301-822-29 (1-11447)

QY 50 SerSerLeuValTYrThrSerAlaMetProGlyPheProTYrProAlaIleThrAlaIle 69
 DB 6232 AACATGTAATCTGACACCCCTGCACCTGCACCTCATAT---AAATTACTGTATT 6288
 QY 70 AlaAlaTYrArg-----GlyAlaHisLeuArgGlyArgGlyArgThrVal----- 84
 DB 6289 GCTGTTATGAAAGATGAGATGGTGCATTAACAGAAATGGAAGAACTGTGGACTC 6348
 QY 85 -----TYrAsnThrPheArgAlaAlaIle 92
 DB 6349 CTTCCTCCTCAGACATACATCTCTGACGAATGATTAAGATTCAAGGTGACCTGG 6408
 QY 93 ProProProProlIleProAlaTYrGlyGlyValTYrGlnGluProValTYrGlyAsn 112
 DB 6409 GATCCTTCACCTCTCTCAGTTCTTGATATAAATAGATATTAACCCAGTGGTTCAT 6468
 QY 113 LysLeuLeuGln-----GlyGlyTYrAlaAlaTYrArgTYrAlaGlnProThrPro 129
 DB 6469 GAGCCCATGGAAGCCTTGTGGAGAAATGACATCATATTAAGCTTACACAATCTCAATCCC 6528
 QY 130 AlaThr 131
 DB 6529 AGCAC 6534

RESULT 10

US-10-177-293-60

Sequence 60, Application US/10177293

Publication No. US20030124128A1

GENERAL INFORMATION:

APPLICANT: Lillie, James
 APPLICANT: Glat, Karen
 APPLICANT: Zhao, Xumel
 APPLICANT: Gannavarpu, Manjula
 APPLICANT: Kamatkar, Shubhang
 APPLICANT: Mertens, Maureen
 APPLICANT: Myer, VIC
 APPLICANT: Wang, Youzhen
 APPLICANT: Xu, Yongyao
 APPLICANT: Hoersch, Sebastian
 APPLICANT: Monahan, John
 APPLICANT: Meyers, Rachel E.
 APPLICANT: Bast Jr., Robert C.
 APPLICANT: Hortobagyl, Gabriel N.
 APPLICANT: Pustel, Lajos
 APPLICANT: Meric, Funda
 APPLICANT: Sahin, Aysegul
 APPLICANT: Mills, Gordon B.
 TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST CANCER
 FILE REFERENCE: MRI-038
 CURRENT APPLICATION NUMBER: US/10/177,293
 CURRENT FILING DATE: 2002-06-21
 PRIOR APPLICATION NUMBER: US 60/299,887
 PRIOR FILING DATE: 2001-06-21
 PRIOR APPLICATION NUMBER: US 60/301,572
 PRIOR FILING DATE: 2001-06-27
 PRIOR APPLICATION NUMBER: US 60/306,501
 PRIOR FILING DATE: 2001-07-18
 PRIOR APPLICATION NUMBER: US 60/325,002
 PRIOR FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: US 60/362,585
 PRIOR FILING DATE: 2002-03-05
 PRIOR APPLICATION NUMBER: US 60/xxx,xxx
 PRIOR FILING DATE: 2002-05-14
 NUMBER OF SEQ ID NOS: 506
 SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 60
 LENGTH: 11447
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-177-293-60

Alignment Scores:

| Pred. No.: | Score: | Length: | Matches: | Conservative: | Mismatches: | Indels: | Gaps: |
|------------------------|--------|---------|----------|---------------|-------------|---------|-------|
| 2,46 | 92.50 | 11447 | 28 | 39.22% | 41 | 21 | 4 |
| Percent Similarity: | 39.22% | | | | | | |
| Best Local Similarity: | 27.45% | | | | | | |
| Query Match: | 11.62% | | | | | | |

US-09-809-545a-2_COPY_1_148 (1-148) x US-10-177-293-60 (1-11447)

QY 50 SerSerLeuValTYrThrSerAlaMetProGlyPheProTYrProAlaIleThrAlaIle 69
 DB 6232 AACATGTAATCTGACACCCCTGCACCTGCACCTCATAT---AAATTACTGTATT 6288
 QY 70 AlaAlaTYrArg-----GlyAlaHisLeuArgGlyArgGlyArgThrVal----- 84
 DB 6289 GCTGTTATGAAAGATGAGATGGTGCATTAACAGAAATGGAAGAACTGTGGACTC 6348
 QY 85 -----TYrAsnThrPheArgAlaAlaIle 92
 DB 6349 CTTCCTCCTCAGACATACATCTCTGACGAATGATTAAGATTCAAGGTGACCTGG 6408
 QY 93 ProProProProlIleProAlaTYrGlyGlyValTYrGlnGluProValTYrGlyAsn 112
 DB 6409 GATCCTTCACCTCTCTCAGTTCTTGATATAAATAGATATTAACCCAGTGGTTCAT 6468
 QY 113 LysLeuLeuGln-----GlyGlyTYrAlaAlaTYrArgTYrAlaGlnProThrPro 129
 DB 6469 GAGCCCATGGAAGCCTTGTGGAGAAATGACATCATATTAAGCTTACACAATCTCAATCCC 6528
 QY 130 AlaThr 131
 DB 6529 AGCAC 6534

RESULT 11

US-10-177-293-62

Sequence 62, Application US/10177293

Publication No. US20030124128A1

GENERAL INFORMATION:

APPLICANT: Lillie, James
 APPLICANT: Glat, Karen
 APPLICANT: Zhao, Xumel
 APPLICANT: Gannavarpu, Manjula
 APPLICANT: Kamatkar, Shubhang
 APPLICANT: Mertens, Maureen
 APPLICANT: Myer, VIC
 APPLICANT: Wang, Youzhen
 APPLICANT: Xu, Yongyao
 APPLICANT: Hoersch, Sebastian
 APPLICANT: Monahan, John
 APPLICANT: Meyers, Rachel E.
 APPLICANT: Bast Jr., Robert C.
 APPLICANT: Hortobagyl, Gabriel N.
 APPLICANT: Pustel, Lajos
 APPLICANT: Meric, Funda
 APPLICANT: Sahin, Aysegul
 APPLICANT: Mills, Gordon B.
 TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST CANCER
 FILE REFERENCE: MRI-038
 CURRENT APPLICATION NUMBER: US/10/177,293
 CURRENT FILING DATE: 2002-06-21
 PRIOR APPLICATION NUMBER: US 60/299,887
 PRIOR FILING DATE: 2001-06-21
 PRIOR APPLICATION NUMBER: US 60/301,572
 PRIOR FILING DATE: 2001-06-27
 PRIOR APPLICATION NUMBER: US 60/306,501

;; PRIOR FILING DATE: 2001-07-18
;; PRIOR APPLICATION NUMBER: US 60/325,002
;; PRIOR FILING DATE: 2001-09-25
;; PRIOR APPLICATION NUMBER: US 60/362,585
;; PRIOR FILING DATE: 2002-03-05
;; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
;; PRIOR FILING DATE: 2002-05-14
;; NUMBER OF SEQ ID NOS: 506
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 62
;; LENGTH: 11560
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc.feature
;; LOCATION: 10981
;; OTHER INFORMATION: n = A,T,C or G
US-10-177-293-62

Alignment Scores:
Pred. No.: 2.49 Length: 11560
Score: 92.50 Matches: 28
Percent Similarity: 39.22% Conservative: 12
Best Local Similarity: 27.45% Mismatches: 41
Query Match: 11.62% Indels: 21
Gaps: 4

US-09-809-545a-2_COPY_1_148 (1-148) x US-10-177-293-62 (1-11560)

QY 50 SerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAlaThAlaAla 69
Db 6345 AACAAATGTAATACGACGCCCTCGCAACCTGACATCCATAT---AAATATACGTATT 6401
QY 70 AlaAlaTyrArg-----GlyAlaHisLeuArgGlyArgGlyArgThVal----- 84
Db 6402 GCTGTTATGAAATGAGATGGATGGCCATCTACAGAAATGGAAGAACTGTGGACATC 6461
QY 85 -----TyrAsnThrPheArgAlaAlaAla 92
Db 6462 CTTCCTCCTCAGAACATACACATCTCGACGAATGATATACAAATTCAGGGTCTCTGG 6521
QY 93 ProProProProLeProAlaTyrGlyGlyValValTyrGlnGluProValTyrGlyAsn 112
Db 6522 GATCCTTACCTTCTCCAGTCTTGATATATAATAGATATATACAGCAGTGGTCCAAAT 6581
QY 113 LysLeuLeuGln-----GlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrPro 129
Db 6582 GAGCCCATGGAAGCCTTTGTTGGAAATGACATCATATACCTTACACAAATCTCAATCCC 6641
Y 130 AlaThr 131
Db 6642 AGCAC 6647

RESULT 12
US-10-198-846-11039
;; Sequence 11039, Application US/10198846
;; Publication No. US2003009974A1
;; GENERAL INFORMATION:
;; APPLICANT: Lillie, James
;; APPLICANT: Xu, Yongyao
;; APPLICANT: Wang, Youzhen
;; APPLICANT: Steinmann, Kathleen
;; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
;; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;; TITLE OF INVENTION: THERAPY OF BREAST CANCER
;; FILE REFERENCE: MRI-049
;; CURRENT APPLICATION NUMBER: US/10/198, 846
;; CURRENT FILING DATE: 2002-07-18
;; PRIOR APPLICATION NUMBER: 60/306,220
;; PRIOR FILING DATE: 2001-07-18
;; NUMBER OF SEQ ID NOS: 14084
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 11039

;; LENGTH: 11657
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc.feature
;; LOCATION: 1, 2, 3, 4, 11656, 11657
;; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-11039

Alignment Scores:
Pred. No.: 2.51 Length: 11657
Score: 92.50 Matches: 28
Percent Similarity: 39.22% Conservative: 12
Best Local Similarity: 27.45% Mismatches: 41
Query Match: 11.62% Indels: 21
Gaps: 4

US-09-809-545a-2_COPY_1_148 (1-148) x US-10-198-846-11039 (1-11657)

QY 50 SerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAlaThAlaAla 69
Db 6398 AACAAATGTAATACGACGCCCTCGCAACCTGACATCCATAT---AAATATACGTATT 6454
QY 70 AlaAlaTyrArg-----GlyAlaHisLeuArgGlyArgGlyArgThVal----- 84
Db 6455 GCTGTTATGAAATGAGATGGATGGCCATCTACAGAAATGGAAGAACTGTGGACATC 6514
QY 85 -----TyrAsnThrPheArgAlaAlaAla 92
Db 6515 CTTCCTCCTCAGAACATACACATCTCGACGAATGATATACAAATTCAGGGTCTCTGG 6574
QY 93 ProProProProLeProAlaTyrGlyGlyValValTyrGlnGluProValTyrGlyAsn 112
Db 6575 GATCCTTACCTTCTCCAGTCTTGATATATAATAGATATATACAGCAGTGGTCCAAAT 6634
QY 113 LysLeuLeuGln-----GlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrPro 129
Db 6635 GAGCCCATGGAAGCCTTTGTTGGAAATGACATCATATACCTTACACAAATCTCAATCCC 6694
QY 130 AlaThr 131
Db 6695 AGCAC 6700

RESULT 13
US-09-996-634-62
;; Sequence 62, Application US/09996634
;; Patent No. US20020172684A1
;; GENERAL INFORMATION:
;; APPLICANT: Nano, Francis
;; APPLICANT: Mycobacterium Tuberculosis DNA Sequences Encoding
;; TITLE OF INVENTION: Immunostimulatory Peptides
;; TITLE OF INVENTION: Immunostimulatory Peptides
;; FILE REFERENCE: 61260
;; CURRENT APPLICATION NUMBER: US/09/996, 634
;; CURRENT FILING DATE: 2001-11-28
;; PRIOR APPLICATION NUMBER: 09/447,135
;; PRIOR FILING DATE: 2000-01-03
;; PRIOR APPLICATION NUMBER: 08/990,823
;; PRIOR FILING DATE: 1997-12-15
;; PRIOR APPLICATION NUMBER: US 96/10375
;; PRIOR FILING DATE: 1996-06-14
;; PRIOR APPLICATION NUMBER: 60/000,254
;; PRIOR FILING DATE: 1995-06-15
;; NUMBER OF SEQ ID NOS: 169
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 62
;; LENGTH: 821
;; TYPE: DNA
;; ORGANISM: Mycobacterium tuberculosis
;; FEATURE:
;; NAME/KEY: misc.feature
;; LOCATION: (1)-(821)
;; OTHER INFORMATION: n is a, c, g, or t/u.
US-09-996-634-62

| | |
|------------------------|--------|
| Alignment Scores: | |
| Pred. No.: | 0.143 |
| Score: | 91.00 |
| Percent Similarity: | 80.85% |
| Best Local Similarity: | 23.948 |
| Query Match: | 11.43% |
| DB: | 10 |
| | |
| length: | 821 |
| Matches: | 45 |
| Conservative: | 13 |
| Mismatches: | 76 |
| Indels: | 54 |
| Gaps: | 6 |

US-09-809-545A-2_COPY_1_148 (1-148) x US-09-996-634-62 (1-821)

[illegible]

```

RESULT 14
US-09-997-182-62
; Sequence 62, Application US/09997182
; Publication No. US2003049263A1
; GENERAL INFORMATION:
; APPLICANT: Nano, Francis
; TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
; TITLE OF INVENTION: Immunostimulatory Peptides
; FILE REFERENCE: 61258
; CURRENT APPLICATION NUMBER: US/09/997,182
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 09/447,135
; PRIOR FILING DATE: 2000-01-03
; PRIOR APPLICATION NUMBER: 08/990,823
; PRIOR FILING DATE: 1997-12-15
; PRIOR APPLICATION NUMBER: US 96/10375
; PRIOR FILING DATE: 1996-06-14
; PRIOR APPLICATION NUMBER: 60/000,254
; PRIOR FILING DATE: 1995-06-15
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62

```

```

:
: LENGTH: 821
: TYPE: DNA
: ORGANISM: Mycobacterium tuberculosis
:
: FEATURE:
: NAME/KEY: misc-feature
: LOCATION: (1)..(821)
: OTHER INFORMATION: n is a, c, g, or t/u
:
: OS-09-997-182-62

```

| | |
|------------------------|--------|
| Alignment Scores: | |
| pred. No.: | 0.143 |
| Score: | 91.00 |
| Percent Similarity: | 30.85% |
| Best Local Similarity: | 23.94% |
| Query Match: | 11.43% |
| DB: | 11 |
| | |
| length: | 821 |
| Matches: | 45 |
| Conservative: | 13 |
| Mismatches: | 76 |
| Indels: | 5 |
| Gaps: | 64 |

US-09-809-545A-2_COPY_1_148 (1-148) x US-09-997-182-62 (1-821)

| | | | |
|----|-----|---|-----|
| Oy | 1 | MetThrAsnIuylsAlaValAsnProtyrThrAsnGlyTyrPlyIleuAsnProVal | 20 |
| | | | |
| Db | 70 | ATGGCCGACACACTGCTGGCCCGAGCCCGACCCCAAGCCGAGCTGCAACCGGTTCCG | 123 |
| | | | |
| Oy | 21 | GlyAlaValAlaTyrSerProAspPheTyrAlaGlyThrValLeuLeuCySGlnAlaAsnGln | 40 |
| | | | |
| Db | 130 | GCGCAGGCGTTCGGACCGGACGGAGCGTGGGGGTATCAGTCCGTCGCTTCAAAACCG | 189 |
| | | | |
| Oy | 41 | GluglySerSerMetTyrSerIlyProSer | 54 |
| | | | |
| Db | 190 | AGGGCGTGGCGGAGCACTCAAGTCTCCGACCCCGGTGTCTCCAAACCGGCGTGTCAAC | 248 |
| | | | |
| Oy | 55 | ThrSerAlaMetProGlyPheProTyrProAlaAlaThrAlaAlaAlaTyrAlaGly | 74 |
| | | | |
| Db | 250 | TCCGATGCTGTCGCCCAACAACCCAGCCGATCACCAGCTCGCGGGACCCCGCGA | 309 |
| | | | |
| Oy | 74 | | 74 |
| Db | 310 | GGGAGAGGCCCCGGATGCGGATNCAACGGGTTCNMGCGGCGCTCCGCTTCNGATTGA | 368 |
| | | | |
| Oy | 75 | -----AlaHisIleuAlaGlyArg-----GlyArgThrValTyr | 85 |
| | | | |
| Db | 370 | CCCGGACAGTACCCCGGTATGGGACGCTACGCGGAGAAACAACCTGGCGCCGACGGCCAC | 428 |
| | | | |
| Oy | 86 | AsnThrPheArgAlaAlaAlaProProProIleProAlaTyrGlyGlyValValTyr | 105 |
| | | | |
| Db | 430 | CTGGCGCTGTGTACCACTTACCGCCCCGACGCGCGGACCGCGCTGGTGT----- | 488 |
| | | | |
| Oy | 106 | GlnGluProValTyrGlyAsnIys-----LeuLeuGlnGlyGly----- | 118 |
| | | | |
| Db | 481 | -----GTTTCCGGGGCGGGCCCATCTGGTCTTCACAAAGAGGAGCGCGATTCATCTA | 534 |
| | | | |
| Oy | 119 | -----TyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr | 131 |
| | | | |
| Db | 535 | CGGCCAGTCCCTGAACCTGACAGTGGGGCGTCACCGCCGAGCGGCCCATCAGCCACT | 594 |
| | | | |
| Oy | 132 | AlaAlaAlaTyrSerAspSerTyr | 139 |
| | | | |
| Db | 595 | GGGCGAGTATTTTCGATCGACAT | 618 |

```

RESULT 15
US-09-997-181-62
; Sequence 62, Application US/09997181
; Publication No. US20030049269A1
; GENERAL INFORMATION:
; APPLICANT: Nao, Francis
; TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
; TITLE OF INVENTION: Immunostimulatory Peptides
; FILE REFERENCE: 61257
; CURRENT APPLICATION NUMBER: US/09/997,181
; PRIOR APPLICATION NUMBER: 09/447,135
; PRIOR FILING DATE: 2000-01-03
; PRIOR APPLICATION NUMBER: 08/990,823

```


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Query Match: 93.30% Indels: 0
DB: 10 Gaps: 0
US-09-809-545A-1_COPY_535_1143 (1-609) x US-09-809-545A-2 (1-203)

QY 1 ATGACTATATAAAGCCGCTACACCAATGGCTGGAATTAATTCACCTGTG 60
DB 1 MethrasnLysLysAlaValAsnProTyrThrAsnGlyTrpLysLeuAsnProValAl 20
QY 61 GCGCGGTCTACAGCCCGCACTTCTATGAGCAGCGGTGTGTGCGAGCCAAACAG 120
DB 21 GlyAlaValIlyrSerProAspPheTyrAlaGlyThrValLeuLeuGlyGlnAlaAsnGln 40
QY 121 GAGGATCTTCATGTATACAGTGGCCCACTTCTATGTATATCTTGTGCAATGGCTGCG 180
DB 41 GluglySerSerMetTyrSerProAspPheTyrAlaGlyThrValLeuLeuGlyGlnAlaAsnGln 60
QY 181 TTTCCATATCCGCGCCGCACTGTCTACAGTGGTATACAGGAGGCTTCAGAGCGCT 240
DB 61 PheProTyrProAlaAlaIleThrAlaAlaIleTyrAlaGlyAlaIleLeuAlaTrpGlyAlaTrp 80
QY 241 GATCGACCGGTGTATACAGCACTTCTACAGCTGGCGCCCGCCCAATCCCGGCTAT 300
DB 81 GlyArgThrValIlyrAsnThrPheArgAlaAlaIleProProProIleProAlaIlyr 100
QY 301 GCGGAGTAGTGTATCAAGAGCCAGCTGTATGGCAATTAATGCTACAGGTTGCTACGCT 360
DB 101 GlyGlyValIlyrValGlnIleProValIlyrGlyAsnLysLeuLeuGlnGlyIlyrAla 120
QY 361 GCATACCGCTACGCGCCAGCCCACTGTCTGCTGCTACAGTGGTATACAGG 420
DB 121 AlaTyrAlaGlyTyrAlaGlnProThrProAlaThrAlaAlaIleTyrSerAspSerTyrIly 140
QY 421 CGAGTTATGTGTCCGACCCCTTACACACACACTTGTCTCCAGCCCGCCAGCTACGCGCT 480
DB 141 ArgValIlyrAlaAlaAspProTyrThrIleAsnThrLeuAlaProAlaProThrIlyrAla 160
QY 481 GGTGCGATGAATGCTTTTGGCGCCTTGACCGATGCCAAGACTAGAGCCATGCTGATAT 540
DB 161 GlyAlaMetAlaAlaIlePheAlaProLeuThrAspAlaIlyrThrArgSerHisAlaAsp 180
QY 541 GTGGGTCGTTCTTCTTTCATGAGGCTAGTATATGCCAAGGGGAGTACACCGCTTT 600
DB 181 ValGlyLeuValIleuSerSerLeuGlnAlaSerIleTyrGlnGlyIlyrAlaAsnArgPhe 200
QY 601 GCTCCATAT 609
DB 201 AlaProTyr 203

RESULT 2
US-09-794-591-2
; Sequence 2, Application US/09794591
; Patent No. US20010018198A1
; GENERAL INFORMATION:
; APPLICANT: Puist, Stefan M.
; APPLICANT: Shibata, Hiroki
; TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
; TITLE OF INVENTION: Products Related Thereto and Methods of Using Same
; FILE REFERENCE: CE 3093
; CURRENT APPLICATION NUMBER: US/09/794,591
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/145,391
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-591-2

Alignment Scores: 1.36e-47 Length: 330
* Pred. No.: 330

Score: 624.00 Matches: 119
Percent Similarity: 89.78% Conservative: 4
Best Local Similarity: 86.86% Mismatches: 12
Query Match: 53.61% Indels: 2
DB: 9 Gaps: 0
US-09-809-545A-1_COPY_535_1143 (1-609) x US-09-794-591-2 (1-330)

QY 1 ATGACTATATAAAGCCGCTACACCAATGGCTGGAATTAATTCACCTGTG 60
DB 166 MethrasnLysLysThrValAsnProTyrThrAsnGlyTrpLysLeuAsnProValAl 215
QY 61 GCGCGGTCTACAGCCCGCACTTCTATGAGCAGCGGTGTGTGCGAGCCAAACAG 120
DB 216 GlyAlaValIlyrSerProGlyIlePheTyrAlaGlyThrValLeuLeuGlyGlnAlaAsnGln 235
QY 121 GAGGATCTTCATGTATACAGTGGCCCACTTCTATGTATATCTTGTGCAATGGCTGCG 180
DB 236 GluglySerSerMetTyrSerProAspPheTyrAlaGlyThrValLeuLeuGlyGlnAlaAsnGln 255
QY 181 TTTCCATATCCGCGCCGCACTGTCTACAGTGGTATACAGGAGGCTTCAGAGCGCT 240
DB 256 PheProTyrProAlaAlaIleThrAlaAlaIleTyrAlaGlyAlaIleLeuAlaTrpGlyAlaTrp 275
QY 241 GGTGCGACCGGTGTATACAGCACTTCTACAGCTGGCGCCCGCCCAATCCCGGCTAT 300
DB 276 GlyArgThrValIlyrAsnThrPheArgAlaAlaIleProProProIleProAlaIlyr 295
QY 301 GCGGAGTAGTGTATCAAGAGCCAGCTGTATGGCAATTAATGCTACAGGTTGCTACGCT 360
DB 296 GlyGlyValIlyrValGlnIleProGlyIlyrIleuThrProCysAlaGlnIleu--TrpIleuGlySc 315
QY 361 GCATACCGCTACGCGCCAGCCCACTGTCTGCTGCTACAGTGGTATACAGG 407
DB 315 yslleProLeuAlaProAlaIlyrProCysHisCysArgCysLeuGln 330

RESULT 3
US-10-359-385-2
; Sequence 2, Application US/10359385
; Publication No. US20030143622A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Alina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/10/359,385
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/176,657
; PRIOR FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1250374
US-10-359-385-2

Alignment Scores: 6.46e-20 Length: 366
Pred. No.: 315.50 Matches: 90
Score: 49.05% Conservative: 13
Percent Similarity: 42.86% Mismatches: 59
Best Local Similarity: 27.10% Indels: 48
Query Match: 12 Gaps: 10
DB: 10

US-09-809-545A-1_COPY_535_1143 (1-609) x US-10-359-385-2 (1-366)

```

QY      1  ATGACATAATAAAGCCGTGAACCCCTACACCAATGCGTGAATAATTAATCCAGTTG 60
      190  MetThrAsnLysMetValThrProTyrAlaAsnGlyTyrPylsEuserProValVal 209
QY      61  GGGCGCGTACAGACCCCGACTTCTATGACAGGACGCGTGTGTGGCCAGGCCAAC--- 117
      210  GlyAlaValTyrGlyProGluLeuTyrAlaAlaSerSerPheGlnAlaSpValSerLeu 229
QY      118  ---CAGAGGAGATCTTCATGATGATACAGTGGCCCGACGTTACCTT-----GTAATTAATTC 168
      230  GlyAsnAspAlaAlaValProLeuSerGlyArgGlyLysLeuThrTyrIleProLeu 249
QY      169  GCAATGCTGCTGCTTCATATCCG---GCCGCCACTGCTGACGCTCATACCGAGGAGCT 225
      250  IleIleProGlyPheProTyrProThrAlaAlaThrThrAlaAlaAlaPheArgGlyAla 269
QY      226  CACCTTCGAGGCGCGTGTGCGACCGCTGACACACCTTCAGAGCTGCGCGCCGACCC 285
      270  HisLeuArgGlyArgGlyArgThrValTyrGlyAlaValArg---AlaValProProThr 288
      286  CCATCCCGCGCTATGCGGAGTATGATCAAGAGCCAGTGTATGGCAATAAATGCTA 345
      289  AlaIleProAlaTyrProGlyValAspMetGln---ProThrAspMetHisSerLeu 307
QY      346  CAGGCTGTTACGCTCATACCGCTACGCCACGCCACCCCTGCACTGCTGCTGCT-- 403
      308  -----LeuGlnProGlnPro--ProLeuLeuGlnProle 318
QY      404  -----ACAGTACAGATTACGACGAGATTATGCTGCCGACCCCTACACACACACA 453
      318  uGlnProLeuThrValThrValMetAlaGlyCysThrGlnProThrProThr----- 335
QY      454  CTGTGTCAGACCCCGACCTACGCGCTTGGTGCATGATAGCTTTTSCGCGCTGACCGAT 513
      336  -----MeCProLeuProle 340
QY      514  GCCAAGACTAGAGCAGCCTGATGATGATGGGTCTGCTTCTTCTTATTCAGAGCTAGT 573
      340  uPro---LeuAlaMetGluLeuAlaLeuTyr-----ArgVal 351
QY      574  ATATTACCAAGGGGATACACCGTTTGG 601
      351  LyrThrGluValAlaThrAlaAspLeu 360
Db

```

RESULT 4

```

US-10-301-822-26
; Sequence 26, Application US/10301822
; Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangt
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MP01-029P2RM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 3063

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-301-822-26
Alignment Scores:
Pred. No.: 0.0724 Length: 3063
Score: 116.00 Matches: 45
Percent Similarity: 34.08% Conservative: 16
Best Local Similarity: 25.14% Mismatches: 54
Query Match: 9.97% Indels: 64
DB: 12 Gaps: 8

```

US-09-809-545a-1_copy_535_1143 (1-609) x US-10-301-822-26 (1-3063)

```

QY      148  AGTTCACTGTATATATCTTCTGCAATGCCGCTTCCATATCCGCGCCGACCTGTCGA 207
      2078  AsnAsnValIleLeuGlnProLeuGlnProAspThrProTyr---LysIleThrValIle 2096
QY      208  GCTGCATACCGA-----GGGCTCACTTCGAGCGCGGTGTCACACCGTG----- 252
      2097  AlaValTyrGluAspGlyAspGlyGlyHisLeuThrGlyAsnGlyArgThrValGlyLeu 2116
      253  -----TACAACACTTCAGAGCTGGCGG 276
QY      2117  LeuProGlnAsnIleHisIleSerAspGluTyrTyrThrArgPheArgValSerTyr 2136
QY      277  CCCCACCCCGCATCCGCGCTATGGCGAGTGTATCAAGACGACGATGTGGCAAT 336
      2137  AspProSerProSerProValLeuGlyTyrLysIleValTyrLysProValGlySerAsn 2156
QY      337  AATTCCTACAG-----GGTGGTACGCTGATACCGCTACGCGCCGACCCGCT 387
      2157  GluProMetGluAlaPheValGlyGluMetThrSerTyrThrLeu----- 2171
QY      388  GCCACTGCTGCTGCTACAGTACAGTACGACGAGATTATGCTGCCAGCCCTTACAC 447
      2171  ----- 2171
QY      448  CACACACTGCTGCAGCCCGACCTACGGGCTTGGTGCATGATAGCTTTGGC----- 501
      2172  HisAsnLeuAsnProSerThrThrTyrAspVal-----AsnValIlyrAlaGlnTyr 2188
QY      502  -----CCCTTGACCGATGCCAAGACTAGAGCCATGCTGATGATG 543
      2189  AspSerGlyLeuSerValProLeuThrAspGlnGlyThrThr----- 2202
QY      544  GCTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 600
      2203  ---LeuTyrLeuAsnValThrAspLeuLysThrTyrGlnIleGlyTyrPaspThrPhe 2220
Db

```

RESULT 5

```

US-10-177-293-61
; Sequence 61, Application US/10177293
; Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lilly, James
APPLICANT: Ghatt, Karen
APPLICANT: Zhao, Xumel
APPLICANT: Ganuvarpu, Manjula
APPLICANT: Kamatkar, Shubhangt
APPLICANT: Mertens, Maureen
APPLICANT: Myer, Vic
APPLICANT: Wang, Youzhen
APPLICANT: Xu, Yongyao
APPLICANT: Hoersch, Sebastian
APPLICANT: Monahan, John
APPLICANT: Meyers, Rachel E.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Hortobagyi, Gabriel N.
APPLICANT: Puzstai, Lajos
APPLICANT: Meric, Funda
APPLICANT: Sahin, Aysegul
APPLICANT: Mills, Gordon B.

```

```

# TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT
# TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
# FILE REFERENCE: MRI-038
# CURRENT APPLICATION NUMBER: US/10/177,293
# PRIOR FILING DATE: 2002-06-21
# PRIOR APPLICATION NUMBER: US 60/299,887
# PRIOR FILING DATE: 2001-06-21
# PRIOR APPLICATION NUMBER: US 60/301,572
# PRIOR FILING DATE: 2001-06-27
# PRIOR APPLICATION NUMBER: US 60/306,501
# PRIOR FILING DATE: 2001-07-18
# PRIOR APPLICATION NUMBER: US 60/325,002
# PRIOR FILING DATE: 2001-09-25
# PRIOR APPLICATION NUMBER: US 60/362,585
# PRIOR FILING DATE: 2002-03-05
# PRIOR APPLICATION NUMBER: US 60/xxx,xxx
# PRIOR FILING DATE: 2002-05-14
# NUMBER OF SEQ ID NOS: 506
# SOFTWARE: FastSeq for Windows Version 4.0
# SEQ ID NO 61
# LENGTH: 3063
# TYPE: PRT
# ORGANISM: Homo sapiens
# US-10-177-293-61

Alignment Scores:
Pred. No.:      0.0724      Length:      3063
Score:          116.00      Matches:     45
Percent Similarity: 34.08%   Conservative: 16
Best Local Similarity: 25.14% Mismatches:    54
Query Match:      9.97%     Indels:      64
DB:               15       Gaps:         8

US-09-809-545A-1_COPY_535_1143 (1-609) x US-10-177-293-61 (1-3063)
Oy      148 ACTGACTGTATATACCTTCTGCATATCGCTTGTCATATCCGGCCAGCTGTCGA 207
Db      2078 AaaAaaValIleLeuInProLeuGlInProAsprhrProtyr---LysIleThValIle 2096
Oy      208 CGTGCATACCga-----GGGGCTACCTTGAGAGCGGTGTCGCCACCGTg----- 252
Db      2097 AlAaValTyrgLuAsPrLyAsRgLyglYlnIsLeuThrgLyAsngIdAtgrThValcIdlyeu 2116
Oy      253 -----TACAACACCTTCAGAGCGGGCG 276
Db      2117 LeuPProGInAsnIleHsIleSeArSpGLuTPryThraGrphearValserTrp 2136
Oy      277 CCCCCAACCCCAATCCCGGCGCTATGGCGGAGTAGTAATGATACAGGCCAGTGTATGSCAAT 336
Db      2137 AsPProSerProSerProvalLeuglYtYrLysIleValTYrlYlpsProvalIGlyserasn 2156
Oy      337 AAATTGCTACg-----GGTGTACGCTGCATACCGGCTACGCCACCCACCCCT 387
Db      2157 GIuPPromEGluAlaPhelValGIyglUmetThSerTyrrThrlau----- 2171
Oy      388 GCCACTGCTGCTGCTACAGTGCACAGTTACGAGCAGAGTTATGCTGCCGACCCCTACAC 447
Db      2171 ----- 2171
Oy      448 CACACACTTGTCTCCACCCCCCACCTACGGCGTTGGTGCATGAATGCTTTTGG----- 501
Db      2172 HIsAsnLeuAsnPProSerThrThrTYrAspVal--AsnValTYrAlaglinTYr 2188
Oy      502 -----CCCTGACGAGAGGCCAAAGACTAGAGCCATGCGATGATGTG 543
Db      2189 AspSerGlyLeuSerValrProLeuthrAspGlnclYthrThr----- 2202
Oy      544 GGTCTCGTCTTCTTCTCATTTGCAGGCGTAGATATACCAAGGCGGATACACCGTTTTT 600
Db      2203 ---LeuTYrLeuAsnValrThraSPeulYrThrTYrcIlnIleGIYTPrAsprThrPhe 2220

```

[illegible]

```
Db      2157  GlnProMetGlnAlaPheValGlyGluMetThrSerThrIleu----- 2171
Qy      388  GCCACGCTGCTGCTGCTACGTAGACAGTACGAGAGTATTGCTGCCGACCCCTACAC 447
Db      2171  -----
Qy      448  CACACATGCTGCTCAGCCCGCCACCTACGCGCTTGTCATGATCTTTGGC----- 501
Db      2172  HisAsnIleuAsnProSerThrThrTyAspVal-----AsnValTyAlaGlnTyr 2188
Qy      502  -----CCCTTGACCGATGCCAGACTAGAGCCATGCTGATGATGTC 543
Db      2189  AspSerGlyLeuSerValProLeuThrAspGlnGlyThr----- 2202
Qy      544  GGTCTGCTCTTCTTCATTCAGCGCTAGATATACCAAGGGATACACCGTTT 600
Db      2203  LeuTyIleuAsnValThrAspLeuLysThrTyrGlnIleGlyThrPaspThrPhe 2220
```

RESULT 7

```
Sequence 1348, Application US/10017161
Publication No. US20030143668A1
GENERAL INFORMATION:
APPLICANT: SUMA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
PRIOR FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1348
LENGTH: 228
TYPE: PRT
ORGANISM: Homo sapiens
US-10-017-161-1348
```

```
Alignment Scores:
Pred. No.: 0.933 Length: 228
Score: 101.50 Matches: 50
Percent Similarity: 37.74% Conservative: 10
Best Local Similarity: 31.45% Mismatches: 61
Query Match: 8.72% Gaps: 38
B: 12 Indels: 11
```

US-09-809-545a-1_COPY_535_1143 (1-609) x US-10-017-161-1348 (1-228)

```
Qy      26  CCAACACCAATGCGCTGAATTAATTCACATTTGGGCGGCTCTACAGCCCGACGT--- 82
Db      10  ProAlaProProThrAlaGsn---MetAspLeuGlnSerLeuGlyThrProAlaPro 28
Qy      83  -----TCAATGAGCGACGAGTGTGTGTCGCGCCACACAGAGGAGATCTTCA 133
Db      29  ProThrCysSerLeuHisLeuGlnSerLeuGlyThrProPro----- 42
Qy      134  TGTACAGTGGCCCGACCTTCACTTGTATATACCTTTCGCAATGCTGGCTTTCATATCCG 193
Db      43  -----AlaProProThrCysSerLeuHisLeuGlnSerLeuSerThrProProAla 59
Qy      194  CCGCGACTGCTGACGTCGATACCGAGGCGCTCAGCCCTGACGCGCTGCGACCTGT 253
Db      60  ProProThrCysSerLeuHisLeuGlnSerLeuSerThrProProAlaProProThrCys 79
Qy      254  ACAAC---CACCTTCAGAGTGGCGGCGCCCGCCACCCCAATCCGCGCTATGGCGAGTAG 310
Db      80  SerLeuHisLeuGlnSerLeuSerThrProProAlaProPro-----ThrCysSe 96
Qy      311  TGTATCAAGAGCCAGTGTATGTCATTAATTTGCTACAGGGTGGTTCAGCTGATACCGCT 370
```

```
Db      96  ValHisLeuGlnSerLeu-----CysThrPro--- 105
Qy      371  ACGCCGACGCCACCCCTGCGCCACCTGCTGCTGCTACAGTACAGTTCAGGAGAGTTATG 430
Db      106  ---ProAlaProPro-----ThrCysSerLeuHisLeuGln-----SerLeuCy 119
Qy      431  CTGCGCGCCCGCTACACACACACTTGTGTCAGCGCCCGCCACCTGCGGCTTGTCG 485
Db      119  StrProProAlaProPro---ThrCys---SerProHisLeuGlnSerLeuGlyCys 135
```

RESULT 8

```
US-10-128-714-8387
Sequence 8387, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Uiang, Bo
APPLICANT: Hu, Wenqi
APPLICANT: Fishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshtkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: Patent In Version 3.1
SEQ ID NO 8387
LENGTH: 919
TYPE: PRT
ORGANISM: Aspergillus fumigatus
US-10-128-714-8387
```

```
Alignment Scores:
Pred. No.: 1.98 Length: 919
Score: 99.00 Matches: 37
Percent Similarity: 39.50% Conservative: 10
Best Local Similarity: 31.09% Mismatches: 59
Query Match: 8.51% Gaps: 13
DB: 15 Indels: 4
```

US-09-809-545a-1_COPY_535_1143 (1-609) x US-10-128-714-8387 (1-919)

```
Qy      169  GCAATGCGCTGCTTTCATATCCGCGCCACCTGCTCAGCTGATACGAGGAGGCTCAC 228
Db      47  AlaTyAlaGlnGlnAlaPheGlnIleGlySerGlyAlaAsnAlaAlaLeuGlnGlyGln 66
Qy      229  CTTCGAGCGCGTGGTGCACCGGTATACACACTTCAAGACTGGCGGCGCCCGCCCA 288
Db      67  LeuProAlaGlyLysSer-----TyGlyAlaTyr-----ProPro 78
Qy      289  ATCCGCGCCATAGGCGAGTATGTCATAGAGCGCATGTATGSCATTAATTCGTACAG 348
Db      79  GlnProGlnAlaAlaGly-----TyGlnGlnProValTyGlyAlaAspProSerGln 96
Qy      349  GGTGTATACGCTGCTACATACCGCTACGCGCCACCGCCCTGCGCTGCTGCTACAGT 408
Db      97  MetAsnAlaAlaAlaProGlyTyThrAlaProValThrProGlyIleAlaGlnMetThr 116
Qy      409  GACATTCAGGAGAGTATTATGCTGCCGAGCCCTACCCACACACACTGCTCCAGCCCG 468
```

```

Db      117 GlnGlnPheGlyAlaMetGlyAlaThrAspPro-----HisLeuMetProPro-GlnPr 134
OY      469 ACCTACGCGCGTGTGCCATGAAATGCTTTTGGCGCCTTGACCGAGTCCAAACTA 523
Db      134 oProGlnAlaValAlaValAlaProGlnAlaProAlaProValProLeuAsnGlnLeu 152

RESULT 9
US-09-919-603-2
: Sequence 2, Application US/09919603
: Patent No. US20020137679A1
: GENERAL INFORMATION:
: APPLICANT: Lawler, John W.
: TITLE OF INVENTION: COMP/TSP-1, COMP/TSP-2 and other TSP
: TITLE OF INVENTION: Chimeric Proteins
: FILE REFERENCE: 1440.1033-007
: CURRENT APPLICATION NUMBER: US/09/919,603
: CURRENT FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: PCT/US00/02482
: PRIOR FILING DATE: 2000-02-01
: PRIOR APPLICATION NUMBER: 60/118,053
: PRIOR FILING DATE: 1999-02-01
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 1168
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-919-603-2

Alignment Scores:
Score, No.: 2,28 Length: 1168
Percent Similarity: 98.50 Matches: 50
Best Local Similarity: 35.55% Conservative: 25
Query Match: 23.70% Mismatches: 66
DB: 8.46% Indels: 71
Gaps: 13

US-09-919-603-2 (1-609) x US-09-919-603-2 (1-1168)
OY      12 AAGGCGGTGAAGCCCTACCAATGCTGGAATTAATCACTGTGGCGCGGTCTA 71
Db      380 GlnGlyTPrSerProTrpAlaGlnTrpThrGlnCysSerValThnCysGlySerGlyThr 399
OY      72 CAGCCCGGACT-----TCATGACAG 91
Db      400 GlnGlnAlaArgGlyAlaArgSerCysAspValThrSerAsnThrCysLeuGlyProSerIleGln 419
OY      92 GCACGGGTGCTGT-----TGTGCCAGGCCACAGAGAGGAT----- 127
Db      420 ThrArgAlaCysSerLeuSerCysAspThrArgIleArgGlnAspGlyGlyTPrSer 439
OY      128 -----CTTCAGTGTACAGTGGCGCCACGTTCACTTAT 160
Db      440 HisTrpSerProTrpSerSerCysSerValThrCysGlyValAlaGlyAsnIle-ThrArgIle 459
OY      161 ATACTCTGCAATGCTGTGCTT---TCATATCCGGCGCCGACATGCTGCAGCTCATACC 217
Db      459 eArgLeuCysAsnSerProValProGlnMetGlyGlyAsnGlySndys----- 474
OY      218 GAGGGCTACCTTCGAGGCGGTGTGCACCGCTGTACACACACTTGAGAGCTGC---GG 274
Db      475 -lysGlySerGly-----ArgIleThrIysAlaCysGlnGln 486
OY      275 CGGCCCGCACCCCAATCCCGGCTATGGCGGAGTAGTATCAAGAGCCAGCTGTATGGCA 334
Db      486 yAlaProCysProIleAspGlyAlaGlyTrp-----SerProTrp- 498
OY      335 ATAAATGCTACAGAGGTGGTACGCTGCATACCGCTACGCCACGCCACCCCTGCACATG 394
Db      499 -----SerProTrpSerAlaCysThrVal-----Th 507
OY      395 CTGCTGCTTACAGTACAGTATACGAGAGTTTATGCTGCCGAGCCCTACCACACAC-- 452
Db      111 :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::

```

```

Db      50  rcysalaglygylilearglunhgrhryalYalsnsberProglunProglunTrygl 527
Qy      453  -----ACTGTC---TCACGCCCCACCTACGCGGTTGGTGCATGATGCTTTTGGC 502
Db      527  ygilyysalacysvalgIyaspvalglnglungrglmetcysasnlyarsersCyspr 547
Qy      503  CCTGACCGATGCCACGACTAGGAGCATGCG 533
Db      547  ovalaspglyCysLeuSer---AsnProCys 556

RESULT 10
US-09-935-384-764
: Sequence 764, Application US/09935384
: Publication No. US2003016526A1
: GENERAL INFORMATION:
: APPLICANT: CHALLITA-EID, PIA
: APPLICANT: HUBERT, RENE
: APPLICANT: RAITANO, ARTHUR
: APPLICANT: AFAF, DANIEL
: APPLICANT: LEVIN, ELANA
: APPLICANT: PARIS, MARY
: APPLICANT: GE, WANGMAO
: APPLICANT: JAKOBOVITZ, AYA
: TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 156P1H4
: TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
: TITLE OF INVENTION: OTHER CANCERS
: FILE REFERENCE: 51158-20033.00
: CURRENT APPLICATION NUMBER: US/09/935,384
: CURRENT FILING DATE: 2001-08-22
: PRIOR APPLICATION NUMBER: 60/227,098
: PRIOR FILING DATE: 2000-08-22
: NUMBER OF SEQ ID NOS: 783
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 764
: LENGTH: 1302
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: GenScan
US-09-935-384-764

Alignment Scores:
Pred. NO.: 3.52 Length: 1302
Score: 96.50 Matches: 38
Percent Similarity: 40.83% Conservative: 11
Best Local Similarity: 31.67% Mismatches: 53
Query Match: 8.25% Indels: 18
DB: 12 Gaps: 4

US-09-809-545A-1(COPY_535_1143 (1-609) x US-09-935-384-764 (1-1302)
Qy      528  GCTCTAGTCTTTCGTCGTCAGGCGGCAAAAGCATTCATGCGACCAAGCCGTAAGT 469
Db      273  ALaalagIyAlagIyAlagIyAlagIyAlagIyAlagIyAlaAlaAlagIyAlaAlagIy 292
Qy      468  GGGGGGTGAGCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 409
Db      293  glylyglyAla-----AlagIyglyAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 307
Qy      408  ACTGTAGCGACAGCAGTGGCAGGCGGTGGCGCGTGAAGCGGTATGCACGTAAACACC 349
Db      308  ThrThrclyAlaAlaAlaAlagIyThrclyThrclyThrclyAlaAlaAlaAlaAlaAla 327
Qy      348  CTGTACCAATTATTGCGCATACACTGCG-----TCTTGATACACTACTCCGCC 301
Db      328  -CysCysThrcysalagIyCysThrclyCysThrclyCysThrclyThrclyAlaThrcly 347
Qy      300  ATTAGCGCGGGATTTGGG-----GGTGGGCGCGCGCACCTCTGAAGG 259
Db      347  rcysalalalalalagIyCysThrclyAlaThrclyThrclyAlaAlaAlaAlaAlaAla 367
Qy      258  GTTGTACACGGTGGAGCACCGCCCTCGAAGGTGAAGCCCTCGGTATGCACCTGC 205

```



```

OY 217 CGAGGGGCTACCTTCGAGCGCGTGCACCGTGTACACACCTTCAGAGCTGGGCG 276
    ||| |||
Db 257 AARGLYLGNHs-----AspTYTYTYTYAsnSerMetGlnGlnTYrThr 272
OY 277 CCCCCACCCCAATCCGGCTATGGCGGAGTAGTATCAAGACCCAGCTGATGGCAAT 336
    ||||| |||||
Db 273 PropioProPhetYrSerGlyTYrGlyThrProTYrAlaAlaAlaThrAlaAlaArgGln 292
OY 337 AATATGCTACAGGAGTGTACCGTGCATACCGCTACGCCAGCCCGCTGCACCTGCT 396
    : : : : : ||| ||||| ||| ||||| : : :
Db 293 AlaIysMetGlnProGlyAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 312
OY 397 GCTGCC----- 402
    ||| : : :
Db 313 AlaSerGlyAsnAsnAsnSerGlnLeuTYrSerSerProTYrAlaGlyTYrAsnAsnPh 332
OY 403 -----TACAGTGACAGTACCGACGAGCTTATGCTGCCGAC 438
    ||| : : : : : ||||| ||||| ||| : : :
Db 333 GlyGlnGlnAspTYrGlyGlyTYrTYrAsnGlnGlnTYrGlyAsnTYrTYrSerProAla 352
    ||| : : : : : ||||| ||||| ||| : : :
OY 439 CCGTACACACACACACTTCTGCTCCAGCCCC-----ACGTACGCGGTGTG--- 483
    ||| : : : : : ||||| ||||| ||| : : :
Db 353 AsnTYrSerProTYrAlaAlaAlaSerSerProSerSerSerAlaSerHisGlyAsnGlyPhe 372
OY 484 GCCATGATGCTTTGGCGCCCTTGACCGATGCCAAGACTAGAGCCATGCT 534
    : : : ||| : : : ||| : : : ||| : : : |||
Db 373 HisValAlaAlaSerSerAsnLeuSerGlnSerProThrAspThrHisSer 389

RESULT 13
US-09-864-761-40976
; Sequence 40976, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 40976
; LENGTH: 168
; TYPE: prt
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011815.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1
; OTHER INFORMATION: EST HUMAN HIT: T70393.1, EVALU 5.00e-17
; OTHER INFORMATION: SWISSPROT HIT: P31794, EVALU 2.10e-01
US-09-864-761-40976

Alignment Scores:
Pred. No.: 3.06 Length: 168
Score: 95.50 Matches: 42
Percent Similarity: 35.22% Conservative: 16
Best Local Similarity: 26.42% Mismatches: 50
Query Match: 8.20% Indels: 53
DB: Gaps: 11

US-09-809-545A-1_COPY_535_1143 (1-609) x US-09-864-761-40976 (1-168)
OY 15 GCGCGTGAACCCCTACACCAATGCTGCAATTA-----TCCAGTGTGGCGCG 65
    ||| : : : ||| ||||| : : : ||| : : :
Db 8 GlyProGlnProGlnProGlyTyrPheGlnHisLysGlyGlyGlyCysArgGlyAs 27
OY 66 GGT-----CTACAGCGCCGACTTCTATGACAGCAGCGGTGTGTGCGCAGCGCA 116
    ||| ||||| ||||| ||| ||| : : : |||
Db 28 GlySerCysLeuGlnHisSerCysLeuLeuTrpHisSerCysLeuLeuProAlaSer 47
OY 117 CCAGGAGGAGTCTTCATGATGACAGTGCGCCCGCATTCCTGTATTACTTCAATAGCC 176
    : : : ||| : : : ||| : : : ||| : : :
Db 48 LysAsnThrVal-----CysSerLys 54
OY 177 TGGCTTTCATATCCGGCCGCGACATGCTGCATACCGAGGGC---TCACCTTCG 233
    : : : ||| : : : ||||| ||||| : : : |||
Db 55 -----AspLeuGlyGly-----CysSerCysThrGlnGlnSerArgAlaProAla 69
OY 234 AGCGCGTGTGCGCACCGGTACAA-----CACCTTCAGAGCTGC 272
    ||||| ||| ||| ||| ||| ||| ||| |||
Db 70 CysSerTrpSerProArgThrGlnGlnGlySerAlaSerSerHisAspLeuLysSerG 89
OY 273 -----GCGCGCCCGCACCCCAATCCGGC----- 296
    ||||| ||||| ||||| ||| ||| ||| |||
Db 90 SerTYrAlaTrpGlyAlaProThrArgGlnLeuGlyArgSerTrpAlaProAlaCysPro 109
OY 297 -----CRAATG-----CGAGTAGTGTATCAAGACCGACAGTGTATGCAATTAAT 341
    ||||| ||||| ||||| ||| ||| ||| |||
Db 110 ArgSerLeuTrpLeuCysGlnAlaHisSerMetGlyArgAlaSerTrpLeuGlnProAla 129
OY 342 GCTACAGGCGTGTACGCTGATACCGCTACCGCCAGCCAGCCCGCTGCAGCTGC 398
    : : : ||| ||||| : : : ||| |||||
Db 130 SerTrpGlnTrp-----ProLeuGlnMetValGlnMetAlaHisCysGly 144

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RESULT 14
US-09-919-770-4
; Sequence 4, Application US/09919770
; Patent No. US20020048577A1
; GENERAL INFORMATION:

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:
: APPLICANT: Bornstein, Paul
: APPLICANT: Kyriakides, Themis
: APPLICANT: Ratner, Buddy
: APPLICANT: Giachelli, Cecilia
: APPLICANT: Martinson, Laura
: APPLICANT: Scalena, Marta
: TITLE OF INVENTION: Methods and Devices to Modulate the Wound Response
: FILE REFERENCE: US06117618
: CURRENT APPLICATION NUMBER: US/09/919,770
: PRIOR FILING DATE: 2001-07-31
: PRIOR APPLICATION NUMBER: US 60/222,071
: PRIOR FILING DATE: 2000-08-01
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 4
: LENGTH: 1172
: TYPE: prt
: ORGANISM: Homo Sapien
US-09-919-770-4

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Oy 503 CCTGACCGATGCCAAGACTAGAGCCATGC 533
::||| ||| ||| |||
Db 549 ovalaspGlyCysLeuser---AsnProCys 558

Search completed: September 25, 2003, 12:06:50
Job time : 284.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 25, 2003, 11:46:54 : Search time 53 Seconds
(without alignments)
5071.742 Million cell updates/sec

Title: US-09-809-545A-1_COPY_535_1143

Perfect score: 609
Sequence: 1 atgactataataaagccgt.....acaacgctttgtctcatat 609

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Optical number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/prodata/1/lna/5A_COMB.seq:*
2: /cgn2_6/prodata/1/lna/5B_COMB.seq:*
3: /cgn2_6/prodata/1/lna/6A_COMB.seq:*
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5: /cgn2_6/prodata/1/lna/PCUTUS_COMB.seq:*
6: /cgn2_6/prodata/1/lna/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|---------|-------|---|
| 1 | 428.6 | 70.4 | 2372 | 3 | US-09-145-391-1 Sequence 1, Appl1 |
| 2 | 63.2 | 10.4 | 1506 | 3 | US-09-176-657-5 Sequence 5, Appl1 |
| 3 | 63.2 | 10.4 | 1506 | 4 | US-09-421-299-5 Sequence 5, Appl1 |
| 4 | 37.4 | 6.1 | 7218 | 1 | US-08-232-463-14 Sequence 14, Appl1 |
| 5 | 37 | 6.1 | 4411529 | 3 | US-09-103-840A-1 Sequence 1, Appl1 |
| 6 | 36.8 | 6.0 | 31571 | 1 | US-08-323-443B-1 Sequence 1, Appl1 |
| 7 | 36.4 | 6.0 | 4403765 | 3 | US-09-103-840A-2 Sequence 2, Appl1 |
| 8 | 36.4 | 6.0 | 4411529 | 3 | US-09-103-840A-1 Sequence 1, Appl1 |
| 9 | 35.6 | 5.8 | 4403765 | 3 | US-09-103-840A-2 Sequence 2, Appl1 |
| 10 | 34.4 | 5.6 | 1278 | 4 | US-09-252-991A-15263 Sequence 15263, A |
| 11 | 34.4 | 5.6 | 1512 | 4 | US-08-402-282-3 Sequence 15311, A |
| 12 | 34.2 | 5.6 | 15664 | 1 | US-08-508-004-3 Sequence 3, Appl1 |
| 13 | 34.2 | 5.6 | 15664 | 1 | US-08-508-004-3 Sequence 3, Appl1 |
| 14 | 34.2 | 5.6 | 15664 | 1 | US-08-402-068-3 Sequence 3, Appl1 |
| 15 | 34.2 | 5.6 | 15664 | 1 | US-08-402-068-3 Sequence 3, Appl1 |
| 16 | 33.4 | 5.5 | 538 | 4 | US-09-056-556-180 Sequence 180, App |
| 17 | 33.4 | 5.5 | 538 | 4 | US-09-072-596-175 Sequence 175, App |
| 18 | 32.8 | 5.4 | 535 | 4 | US-09-056-556-171 Sequence 171, App |
| 19 | 32.8 | 5.4 | 535 | 4 | US-09-072-596-166 Sequence 166, App |
| 20 | 32.2 | 5.3 | 1071 | 2 | US-08-997-080-180 Sequence 180, App |
| 21 | 32.2 | 5.3 | 1071 | 2 | US-08-997-362-180 Sequence 180, App |
| 22 | 32.2 | 5.3 | 1071 | 3 | US-09-095-855-180 Sequence 180, App |
| 23 | 32.2 | 5.3 | 1071 | 4 | US-09-324-542-180 Sequence 180, App |
| 24 | 32.2 | 5.3 | 1071 | 4 | US-09-205-426-180 Sequence 180, App |
| 25 | 31.8 | 5.2 | 610 | 4 | US-09-072-596-293 Sequence 293, App |
| 26 | 31.6 | 5.2 | 418 | 3 | US-09-141-000-6 Sequence 6, Appl1 |
| 27 | 31.4 | 5.2 | 458 | 3 | US-09-141-000-4 Sequence 4, Appl1 |

| | | | | | |
|------|------|-----|------|---|---|
| C 28 | 31.2 | 5.1 | 2558 | 3 | US-08-999-733-3 Sequence 3, Appl1 |
| C 29 | 31.2 | 5.1 | 9757 | 1 | US-08-093-453B-1 Sequence 1, Appl1 |
| C 30 | 31.2 | 5.1 | 9759 | 1 | US-08-459-041A-1 Sequence 1, Appl1 |
| C 31 | 31.2 | 5.1 | 9759 | 3 | US-08-999-733-1 Sequence 1, Appl1 |
| C 32 | 30.6 | 5.0 | 4793 | 4 | US-09-561-497-10 Sequence 10, Appl1 |
| C 33 | 30.4 | 5.0 | 408 | 4 | US-09-252-991A-13491 Sequence 13491, A |
| C 34 | 30.4 | 5.0 | 591 | 4 | US-09-252-991A-13956 Sequence 13956, A |
| C 35 | 30.4 | 5.0 | 1711 | 4 | US-09-620-3120-159 Sequence 159, App |
| C 36 | 30.4 | 5.0 | 2103 | 4 | US-09-252-991A-13604 Sequence 13604, A |
| C 37 | 30.4 | 5.0 | 2259 | 4 | US-09-252-991A-13396 Sequence 13396, A |
| C 38 | 30.4 | 5.0 | 3222 | 4 | US-09-252-991A-13746 Sequence 13746, A |
| C 39 | 30 | 4.9 | 3848 | 3 | US-09-112-096-28 Sequence 28, Appl1 |
| C 40 | 30 | 4.9 | 5610 | 4 | US-09-262-537-57 Sequence 57, Appl1 |
| C 41 | 30 | 4.9 | 5668 | 3 | US-09-112-096-14 Sequence 14, Appl1 |
| C 42 | 29.8 | 4.9 | 744 | 3 | US-09-385-028-22 Sequence 22, Appl1 |
| C 43 | 29.8 | 4.9 | 744 | 4 | US-09-726-614-22 Sequence 22, Appl1 |
| C 44 | 29.8 | 4.9 | 2283 | 3 | US-09-153-804-5 Sequence 5, Appl1 |
| C 45 | 29.8 | 4.9 | 2903 | 2 | US-08-310-912A-1 Sequence 1, Appl1 |

ALIGNMENTS

RESULT 1
US-09-145-391-1
Sequence 1, Application US/09145391
Patent No. 6194171.
GENERAL INFORMATION:
APPLICANT: Pulist, Stefan M.
APPLICANT: Shibata, Hiroki
TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
TITLE OF INVENTION: Products Related Thereto and Methods of Using Same
FILE REFERENCE: CE 3093
CURRENT APPLICATION NUMBER: US/09/145,391
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2372
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (987)..(1979)
US-09-145-391-1

Query Match 70.4%; Score 428.6; DB 3; Length 2372;
Best Local Similarity 82.0%; Pred. No. 4.7e-122;
Matches 542; Conservative 0; Mismatches 64; Indels 55; Gaps 2;

| | | | |
|----|------|---|------|
| QY | 1 | ATGACTAATRAAAGGCGGTGAACCCCTACCAATGCTGGAATTAATTCAGTTGTG | 60 |
| DB | 1572 | ATGACAAATRAAAGGCGGTGAACCCCTATACAAAGGCTGGAATTAATTCAGTTGTG | 1631 |
| QY | 61 | GGCGCGGTACAGCCGCTCTATGAGGAGCGGCTGTGTGCCAGGCCAACAG | 120 |
| DB | 1632 | GGGCGAGTCTACAGTCCCAATTCATGACAGGAGCGTCTGTGTGCCAGGCCAACAG | 1691 |
| QY | 121 | GAGGAGTCTTCATGATGAGTGGCCCACTTCACTTGATATATACCTTGCAATGCTGGC | 180 |
| DB | 1692 | GAGGAGTCTTCATGATGAGTGGCCCACTTCACTTGATATATACCTTGCAATGCTGGC | 1751 |
| QY | 181 | TTTCCATATCCGCGCGGCTGTGAGCTGCATACGAGGCGGCTACCTTGAGGCGGT | 240 |
| DB | 1752 | TTTCCATATCCGCGCGGCTGTGAGCTGCATACGAGGCGGCTACCTTGAGGCGGT | 1811 |
| QY | 241 | GGTCGACCGGTGACAACTTCAGAGCTGCGGCGCCCAACCCCAATCCCGGCTAT | 300 |
| DB | 1812 | GGTCGACCGGTGACAACTTCAGAGCTGCGGCGCCCAACCCCAATCCCGGCTAT | 1871 |
| QY | 301 | GCGGAGTATGATGATACAGAGCCAGTATGCAATTAATGCTACAGGCTGATACGCT | 360 |
| DB | 1872 | GCGGAGTATGATGATACAGAGCCAGTATGCAATTAATGCTACAGGCTGATACGCT | 1929 |

| | | | |
|----|------|---|-------|
| OY | 361 | GCATACCGCCTACGGCCACCCACCCCTCCACTGGTGGCTACAGTA----- | 410 |
| Db | 1930 | GCATACCGCCTACGGCCACCCACTCCCTGCTACAGTACAGAAATCAG | 19839 |
| OY | 411 | -----CAGTTACGACAGATT | 427 |
| Db | 1990 | TTGCTCTTTCGTTGACGAGATGAATTTCTTGTAAACCTCTGCAAGTTACGACGAGATT | 2049 |
| OY | 428 | ATGCTGCGCAGCCCTACCCACACACACTTGGCTCAGCCCCACCTACGGCGTTGGTGCA | 487 |
| Db | 2050 | ATGCTGCGCAGCCCTACCCACACAGCACTTGGCTCAGCCCCACCTACGGCGTTGGTGCA | 2109 |
| OY | 488 | TGAAATGCTTTGGCGCCTTGAACCGATGCGCAAGACTAGAGCCATGCTGATATGTGGTC | 547 |
| Db | 2110 | TGAATGCTTTGGCACTTTGACTGTGCGCAAGACTAGAGCCATGCTGATATGTGGCTC | 2169 |
| OY | 548 | TCGTTCTTTCTTCATTGACAGCTAGTATATACCAAGGGGATATACACGTTTGTCCAT | 607 |
| Db | 2170 | TCGTTCTTTCTTCATTGACAGCTAGTATATACCGAGGGGATATACACGTTTGTCCAT | 2229 |
| OY | 608 | A 608 | |
| Db | 2230 | A 2230 | |

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RESULT 2
US-09-176-657-5
; Sequence 5, Application US/09176657
; Patent No. 6020164
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Lu, Aina
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
FILE REFERENCE: PF-0611 US
CURRENT APPLICATION NUMBER: US/09/176,657
CURRENT FILING DATE: 1998-10-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Homo sapiens
FEATURE: _
OTHER INFORMATION: 1250374
-09-176-657-5

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|-----------------------|-------|--------------|-------|------------|-----|--------|------|
| Query Match | 10.4% | Score | 63.2 | DB | 3 | Length | 1506 |
| Best Local Similarity | 54.5% | Pred. No. | 1e-09 | | | | |
| Matches | 279 | Conservative | 0 | Mismatches | 193 | Indels | 40 |
| | | | | | | Gaps | 6 |

[illegible]

| | | | |
|----|------|---|------|
| Db | 1008 | CATTGAGGGGCAGAGGGCGGACAGTAAATAGTGCAGTCCGA-----GGGGTACTCCACA | 1064 |
| QY | 286 | CCATTCGCCGGCTTATGGCGAGTAGTATCAAGACGACAGTATGGCATTAATTGCTA | 345 |
| Db | 1065 | GCCATTTCTTTTCTTTCAGGGGTGGATATGACGGCTCAAGATATGACAGCGCTCTACTG | 1124 |
| QY | 346 | CAGAGTGGTTACGCTGCATACCGGTACGCCACGCCACCCCTGCACATGCTGCTCATC | 405 |
| Db | 1125 | CAAC-----CGCAGCCACCGCTGCTGACGGCGCTGCACGGCGCTTAC | 1165 |
| QY | 406 | AGTGACAGTACGAGACAGTTTATGCTGCGACCCCTTACCAACACACTTGTCTCCAGCC | 465 |
| Db | 1166 | AGTACGGTTATGCGAGGGGTGTACACAGCCACCCCT---ACCATGCCCTTGCCTCGCC | 1222 |
| QY | 466 | CCCACTTACGGCGTTGGTGCATGAAATGCTT | 497 |
| Db | 1223 | GCTAGCTATGGAGTTGGCGCTGTGTGCCAGTTT | 1254 |

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1  RESULT 3
2  US-09-421-299-5
3  ; Sequence 5, Application US/09421299
4  ; Patent No. 6524579
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Bandman, Olga
7  ; APPLICANT: Tang, Y. Tom
8  ; APPLICANT: Corley, Neil C.
9  ; APPLICANT: Guegler, Karl J.
10 ; APPLICANT: Lu, Aina
11 ; APPLICANT: Baugun, Mariah R.
12 ; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
13 ; FILE REFERENCE: PF-0611 US
14 ; CURRENT APPLICATION NUMBER: US/09/421,299
15 ; CURRENT FILING DATE: 1999-10-20
16 ; EARLIER APPLICATION NUMBER: 09/116,657
17 ; EARLIER FILING DATE: 1998-10-21
18 ; NUMBER OF SEQ ID NOS: 9
19 ; SOFTWARE: PERL Program
20 ; SEQ ID NO 5
21 ; LENGTH: 1506
22 ; TYPE: DNA
23 ; ORGANISM: Homo sapiens
24 ; FEATURE: _
25 ; OTHER INFORMATION: 1250374
26 US-09-421-299-5

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| | | | | | | | |
|---------------------------|-------|------------|-------|--------|----|--------|------|
| Query Match | 10.4% | Score | 63.2 | DB | 4 | Length | 1506 |
| Best Local Similarity | 54.5% | Pred. No. | 1e-09 | | | | |
| Matches 279; Conservative | 0 | Mismatches | 193 | Indels | 40 | Gaps | 6 |

Oy 1 TTGCATATAAAAAAGGCGGTACACCCCTACACCAAGGCTGGAAATTAAATCAAGTTGTG 60
 Db ATGCACCAATTAAGAAAGATGCTCACACCCATATGCAAATGTTGGAAATTAAGCCCAAGTATT 827
 Oy 61 GGCGCGGTCTACAGCCGCCGACTTCTATGCAGGACGGGTGCT-----TGTGCAG 111
 Db GGACCTGATATGTTGGTCCGGAGTTATATGCAGCATCCAGCTTTCAAGCAGATGTTCCCTA 887
 Oy 112 GCCAACGAGAGGAGATCTTCCATGTATACAGTGGCCCCAGTTCATCTTATATACTTTCGA 171
 Db GGCAATGATGACGACAGTGGCCCTATACGAAGAGGGGTAATCAACACTTACATCTCTTTA 947
 Oy 172 ---ATGCCGTGGCTTCCATA---TCGGCGCGCCACTGCTGCAGCTGCATATCCAGGGGCT 225
 Db ATCATCTCTGGCTTCCCTTACCTTACCTACGACGCCACCGCAGCGCTTCACAGGAGGCC 1007
 Oy 226 CACCTTGAAGGCCCTGTGTGCACCGTGTACAAACCTTCAGAGGCTGGGGGCGCCCCACCC 285
 Db CATTTGAGGGGCAAGGGCGGACAGTATATGTCAGTCCGA---GGGTAACCTCCACAA 1064
 Oy 286 CCATATCCCGGCTATGGCGAGTAGTGTATCAACAGCCAGGTATGGCATAAATTCTA 345
 Db GCCATCCCGGCTATTCACAGGGGTGGAATATGACGCTTACAGATATGACACAGCTGCTACTG 1124

| | | | | |
|---------------------------|--------|-----------------|-----------|-----------------|
| Query Match | 5.8% | Score 35.6; | DB 3; | length 4403765; |
| Best Local Similarity | 43.6%; | Pred. No. 11; | | |
| Matches 158; Conservative | 0; | Mismatches 204; | Indels 0; | Gaps 0 |

```

: NUMBER OF SEQ ID NOS: 33142
: SEQ ID NO 15263
: LENGTH: 1278
: TYPE: DNA
: ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15263

Query Match          5.6%; Score 34.4; DB 4; Length 1278;
Best Local Similarity 50.6%; Pred. No. 0.7;
Matches 83; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

OY 341 TGTACAGAGGTGGTTAGCGTCGATACCGCTACGCCACCCACCCCTGCCACTGCTGCTG 400
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 603 TGTCTCAGCAGAGTTGTGTGGCGCGCCAGCACGGCCGGCGACAGAGTGCGCTGCCCGG 544
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 401 CCTCAGAGCAGATTGACGGAGAGTTATGCTGGCGACCCCTACACACACTTGCTC 460
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 543 GCGACGATGACGATGGCGGCTTGTGCTGCTGTGCTGACACGATGACGACGCCACCCGCTG 484
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 461 CAGCCCCCACCCTACGGCGGTGGTGCATGATGCTTTTGCGCCC 504
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 483 GACTCCCGCGCCACCCCGCTGCAGCCCTGGCAGTCATGCGCCTC 440
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
US-09-252-991A-15311/c
: Sequence 15311, Application US/09252991A
: Patent No. 6551795
: GENERAL INFORMATION:
: APPLICANT: Marc J. Rubenfield et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
: FILE REFERENCE: 107196.136
: CURRENT APPLICATION NUMBER: US/09/252.991A
: CURRENT FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
: PRIOR FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27
: NUMBER OF SEQ ID NOS: 33142
: SEQ ID NO 15311
: LENGTH: 1512
: TYPE: DNA
: ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15311

Query Match          5.6%; Score 34.4; DB 4; Length 1512;
Best Local Similarity 50.6%; Pred. No. 0.75;
Matches 83; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

OY 341 TGTACAGAGGTGGTTAGCGTCGATACCGCTACGCCACCCACCCCTGCCACTGCTGCTG 400
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RESULT 12
US-08-402-282-3
: Sequence 3, Application US/08402282
: Patent No. 5476768
: GENERAL INFORMATION:
: APPLICANT: Pearson, Robert E.
: APPLICANT: Dickinson, Julie A.
: APPLICANT: Hamilton, Paul T.
: APPLICANT: Little, Michael C.
: APPLICANT: Beyer Jr., Wayne F.

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1  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
2  TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
3  FILE REFERENCE: 107196.136
4  CURRENT APPLICATION NUMBER: US/09/252,991A
5  CURRENT FILING DATE: 1999-02-18
6  PRIOR APPLICATION NUMBER: US 60/074,788
7  PRIOR FILING DATE: 1998-02-18
8  PRIOR APPLICATION NUMBER: US 60/094,190
9  PRIOR FILING DATE: 1998-07-27
10 NUMBER OF SEQ ID NOS: 33142
11 SEQ ID NO: 15311
12 LENGTH: 1512
13 TYPE: DNA
14 ORGANISM: Pseudomonas aeruginosa
15 US-09-252-991A-15311
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18 Best Local Similarity 50.6%; Pred. No. 0.75;
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33 RESULT 12
34 ; Sequence 3, Application US/08402282
35 ; Patent No. 5476768
36 ; GENERAL INFORMATION:
37 ; APPLICANT: Pearson, Robert E.
38 ; APPLICANT: Dickson, Julie A.
39 ; APPLICANT: Hamilton, Paul T.
40 ; APPLICANT: Little, Michael C.
41 ; APPLICANT: Beyer Jr., Wayne F.

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? TITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE
? TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX
? NUMBER OF SEQUENCES: 6
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
? STREET: 1 Becton Drive
? CITY: Franklin Lakes
? STATE: NJ
? COUNTRY: US
? ZIP: 07417
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/402,282
? FILING DATE:
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Fugit, Donna R.
? REGISTRATION NUMBER: 32,135
? REFERENCE/DOCKET NUMBER: P-3283
? INFORMATION FOR SEQ ID NO: 3:
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DB 900 GGCACACCGCTGTGCGCAGCGCGCAT 926

RESULT 14
US-08-402-066-3

Sequence 3, Application US/08402066
Patent No. 5612182
GENERAL INFORMATION:
APPLICANT: Pearson, Robert E.
APPLICANT: Dickson, Julie A.
APPLICANT: Hamilton, Paul T.
APPLICANT: Little, Michael C.
APPLICANT: Beyer Jr., Wayne F.
TITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE
TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
ADDRESSEE: Company
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: NJ
COUNTRY: US
ZIP: 07417
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,066
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-3283
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15664 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
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Query Match 5.6%; Score 34.2; DB 1; Length 15664;
Best Local Similarity 47.8%; Pred. No. 2.5;
Matches 99; Conservative 0; Mismatches 108; Indels 0; Gaps 0

QY 220 GGGGCTACCTTCAGAGCGCGGTGTCGACCCGTCATCAACACTTCAGAGCTCGGGCGCC 279
Db 720 GGGGCTACCTTCAGAGCGCGGTGTCGATGATCCCGCAGCAATGCAATCGGCTGGCC 779
QY 280 CCACCCCCCAATCCCGGCTATGGGGAAGTAGTATCAAGAGCCAGTAGTGGCAATAA 339
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Db 900 GGCCACACCGTGTGCCAAGCCCGCGAT 926

RESULT 15
US-08-402-068-3
Sequence 3, Application US/08402068
Patent No. 5633159
GENERAL INFORMATION:
APPLICANT: Pearson, Robert E.
APPLICANT: Dickson, Julie A.
APPLICANT: Hamilton, Paul T.
APPLICANT: Little, Michael C.
APPLICANT: Bayer Jr., Wayne F.
TITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE
TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Richard J. Rodrick, Becton Dickinson and
ADDRESS: Company
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: NJ
COUNTRY: US
ZIP: 07417
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,068
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-3283
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

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LENGTH: 15664 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
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| QY | DB | Matches | 99; Conservative | 0; | Mismatches | 108; | Indels |
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Thu Sep 25 13:04:40 2003

us-09-809-545a-1_copy_535_1143.rni

Page 11

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Search completed: September 25, 2003, 11:56:31
Job time : 76 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 25, 2003, 11:39:29 ; Search time 172 Seconds

(without alignments)
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Title: US-09-809-545a-1_COPY_535_1143

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Gapop 10.0 , Gapext 1.0

Searched: 1678620 seqs, 1244745471 residues

Optimal number of hits satisfying chosen parameters: 3357240

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 4 | 63.2 | 10.4 | 1506 | 12 | US-10-359-385-5 |
| 5 | 55.2 | 9.1 | 60 | 12 | US-09-908-975-7420 |
| 6 | 36.8 | 6.0 | 1049 | 12 | US-10-140-472-358 |
| 7 | 36.8 | 6.0 | 1049 | 12 | US-10-141-761-358 |
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| 14 | 35.4 | 5.8 | 440 | 14 | US-10-184-634-202 |
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| C 19 | 34.2 | 5.6 | 594 | 12 | US-10-142-885-10 | Sequence 10, Appl |
| C 20 | 34.2 | 5.6 | 594 | 14 | US-10-123-155-10 | Sequence 10, Appl |
| C 21 | 34.2 | 5.6 | 594 | 15 | US-10-146-731-10 | Sequence 88, Appl |
| C 22 | 34 | 5.6 | 735 | 14 | US-10-184-644-88 | Sequence 88, Appl |
| C 23 | 34 | 5.6 | 735 | 14 | US-10-184-634-88 | Sequence 180, Appl |
| C 24 | 33.4 | 5.5 | 538 | 12 | US-10-084-843-180 | Sequence 175, Appl |
| C 25 | 33.4 | 5.5 | 538 | 12 | US-10-193-002-175 | Sequence 171, Appl |
| C 26 | 32.8 | 5.4 | 535 | 12 | US-10-084-843-171 | Sequence 166, Appl |
| C 27 | 32.8 | 5.4 | 535 | 12 | US-10-193-002-166 | Sequence 166, Appl |
| C 28 | 32.8 | 5.4 | 786 | 14 | US-10-156-761-6751 | Sequence 6751, Ap |
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| C 30 | 32.8 | 5.4 | 3063 | 13 | US-10-027-632-114388 | Sequence 114389, |
| C 31 | 32.8 | 5.4 | 3063 | 13 | US-10-027-632-114389 | Sequence 127378, |
| C 32 | 32.6 | 5.4 | 815 | 13 | US-10-027-632-127378 | Sequence 649, App |
| C 33 | 32.6 | 5.4 | 45191 | 15 | US-10-080-170-649 | Sequence 402, App |
| C 34 | 32.2 | 5.3 | 653 | 14 | US-10-184-644-402 | Sequence 402, App |
| C 35 | 32.2 | 5.3 | 653 | 14 | US-10-184-634-402 | Sequence 3417, Ap |
| C 36 | 32.2 | 5.3 | 951 | 10 | US-09-738-626-3417 | Sequence 180, App |
| C 37 | 32.2 | 5.3 | 1071 | 11 | US-09-880-505-180 | Sequence 24, Appl |
| C 38 | 32.2 | 5.3 | 1071 | 12 | US-10-205-979-24 | Sequence 180, App |
| C 39 | 32.2 | 5.3 | 1071 | 13 | US-10-051-643-180 | Sequence 180, App |
| C 40 | 32.2 | 5.3 | 1185 | 10 | US-09-738-626-3418 | Sequence 3418, Ap |
| C 41 | 32.2 | 5.3 | 3309400 | 10 | US-09-738-626-1 | Sequence 1, Appl1 |
| C 42 | 32 | 5.3 | 696 | 12 | US-10-140-472-354 | Sequence 354, App |
| C 43 | 32 | 5.3 | 696 | 12 | US-10-141-761-354 | Sequence 354, App |
| C 44 | 32 | 5.3 | 696 | 12 | US-10-142-885-354 | Sequence 354, App |
| C 45 | 32 | 5.3 | 696 | 14 | US-10-123-155-354 | Sequence 354, App |

ALIGNMENTS

RESULT 1
US-09-809-545A-1
; Sequence 1, Application US/09809545A
; Patent No. US20020110804A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, Lawrence W.
; TITLE OF INVENTION: SECRETED FACTORS
; FILE REFERENCE: SCIOS.017A
; CURRENT APPLICATION NUMBER: US/09/809,545A
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1340
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-809-545A-1

Query Match 100.0%; Score 609; DB 10; Length 1340;
Best Local Similarity 100.0%; Pred. No. 3.9e+195;
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | |
|----|-----|--|
| QY | 1 | ATGACATTAATAAAGCCGCGTGAACCCCTACCAATGCTGGAAATTAATCAATGTCG 60 |
| DB | 535 | ATGACATTAATAAAGCCGCGTGAACCCCTACCAATGCTGGAAATTAATCAATGTCG 594 |
| QY | 61 | GCGCGGCTACAGCCCGACCTTATGACAGCAGCGTGTGTGCCAGGCAACGAG 120 |
| DB | 595 | GCGCGGCTACAGCCCGACCTTATGACAGCAGCGTGTGTGTGCCAGGCAACGAG 654 |
| QY | 121 | GAGGATCTTCATGATGACAGTGGCCCACTTGTATATACCTTGTCAATGCTGGC 180 |
| DB | 655 | GAGGATCTTCATGATGACAGTGGCCCACTTGTATATACCTTGTCAATGCTGGC 714 |
| QY | 181 | TTTTCATATCCGCGCCGACCTGTCAGCTGCATACGAGGCGCTACCTGAGGCGCT 240 |
| DB | 715 | TTTTCATATCCGCGCCGACCTGTCAGCTGCATACGAGGCGCTACCTGAGGCGCT 774 |

| | | | |
|----|------|--|------|
| OY | 241 | GGTGGACCGGTTCACACACCTTCAGACCTGGGGCCCCACACCCCCCAATCCGGCCAT | 300 |
| | | | |
| Db | 775 | GGTGCACCCGGTATCAACACCTTCAGACCTGGGGCCCCACACCCCAATCCGGCCAT | 834 |
| | | | |
| OY | 301 | GGCGGAGTAGTGTATCAAGAGCAGCAGTGATGGCAATAAATTGCTTCAGAGGTGGTTACGCT | 360 |
| | | | |
| Db | 835 | GGCGGAGTAGTGTATCAAGAGCAGCAGTGATGGCAATAAATTGCTTCAGAGGTGGTTACGCT | 894 |
| | | | |
| OY | 361 | GCATACGCGTACGCCACGCCACCCCTGCACACTGCTGCCTACAGTACAGTTACGGA | 420 |
| | | | |
| Db | 895 | GCAATACCCCTACGCCACGCCACCCCTGCACACTGCTGCCTACAGTACAGTTACGGA | 954 |
| | | | |
| OY | 421 | CGAATTTATGTTGGCGAGACCCCTACACACACACTGCTCCAGACCCCACTAGGGCGTT | 480 |
| | | | |
| Db | 955 | CGAATTTATGTTGGCGAGACCCCTACACACACACTGCTCCAGACCCCACTAGGGCGTT | 1014 |
| | | | |
| OY | 481 | GGTGCATGAATGCTTTTGGCCCTTGACCATGGCAAGACTAGGAGGCATGCTGAT | 540 |
| | | | |
| Db | 1015 | GGTGCATGAATGCTTTTGGCCCTTGACCATGGCAAGACTAGGAGGCATGCTGAT | 1074 |
| | | | |
| OY | 541 | GTGGGCTCGTTCTTCTTCATTTGCAGGCTAGTATATCCAAAGGGGATACAAACGTTTT | 600 |
| | | | |
| Db | 1075 | GTGGGCTCGTTCTTCTTCATTTGCAGGCTAGTATATCCAAAGGGGATACAAACGTTTT | 1134 |
| | | | |
| OY | 601 | GCTCCATAT 609 | |
| | | | |
| Db | 1135 | GCTCCATAT 1143 | |

RESULT 2
 US-09-794-591-1
 : Sequence 1, Application US/097944591
 : Patent No. US20010018198A1
 : GENERAL INFORMATION:
 : APPLICANT: Pulst, Stefan M.
 : APPLICANT: Shibata, Hiroki
 : TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
 : TITLE OF INVENTION: Products Related Thereto and Methods of Using Same
 : FILE REFERENCE: CE 3093
 : CURRENT APPLICATION NUMBER: US/09/794,591
 : CURRENT FILING DATE: 2001-02-26
 : PRIOR APPLICATION NUMBER: 09/145,391
 : PRIOR FILING DATE: 1998-09-01
 : NUMBER OF SEQ ID NOS: 2
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 1
 : LENGTH: 2372
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (987)..(1979)
 : US-09-794-591-1

| | | | | |
|----------------------|----------------|--------------------|-----------|-------------|
| Query Match | 70.4% | Score 428.6 | DB 9 | Length 2372 |
| Best Local Similarly | 82.0% | Pred. No. 4.5e-134 | | |
| Matches 542 | Conservative 0 | Mismatches 64 | Indels 55 | Gaps 2 |

| QY | 1 | ATGACTATATAAAGGCGCTGACACCCCTACACCAATGGCTGGMAATTAAATCCAGTTGTG | 60 |
|----|------|---|------|
| Db | 1572 | ATGCAAAATATAAAGACCGCTCACCCCTTATACAAATGGCTGGAAATTGAATCCAGTTGTG <td>1631</td> | 1631 |
| QY | 61 | GGCGCGGTCTACAGACCCCGACTTCTATACAGACGAGGCGTGTGTGCGACGCCAACAG | 120 |
| Db | 1632 | GGTCCAGTCTACATCCCGAATTCTATACAGGACAGGTCCTGTGTGTGCGACGCCAACAG | 1691 |
| QY | 121 | GAGGGATCTTCATGTACAGTGGCCCAAGTTCACTTGATATATACCTTCGAATGGCTGGC | 180 |
| Db | 1692 | GAGGGATCTTCATGTACAGTGGCCCGCCAGTTCACTTGATATATACCTTCGAATGGCAGGC | 1751 |
| QY | 181 | TTTCCATATCCGGCGCCACCTGCTGCGACGTCATATCCGAGGGGCTCACCTTCGAGGCGCT | 240 |
| Db | 1752 | TTTCCGATATCCAGGACGCGCGCGCGCCCTACACGAGGGGCGACCTTCGAGGCGCGC | 1811 |

| | | | |
|----|------|---|-------|
| QY | 241 | GGTGCACCGCTGTACACACCTTCAGAGACTGGGCGGCCCCACCCCCATCCGGGCTAT | 300 |
| | | | |
| Db | 1812 | GGTCGACCGGTGTACACACCTTCAGGGCGCGGGCGCCCGCCCGATCCGGCCCTAC | 18711 |
| | | | |
| QY | 301 | GGCGAGTAGTGTATCAAGAGCCAGGTGTATGGCAATAATTTGTCACAGGGTGGTTACCT | 360 |
| | | | |
| Db | 1872 | GGCGGTGTGTTTAC--CAGGATGGATTTTATGTGTGACAGCATTTATGGTGGTTATGCT | 19229 |
| | | | |
| QY | 361 | GCATACGGCTACGCCAGCCCAAGCCCTGCGCACTGCTGCTGCCTACAGTGA----- | 410 |
| | | | |
| Db | 1930 | GCATACCGCTACGCCAGCCCAAGCCCTGCGCACTGCGCTGCCTACAGTGAAGAAATCAG | 19899 |
| | | | |
| QY | 411 | -----CAGTAGGAGAGAGTTT | 427 |
| | | | |
| Db | 1990 | TTCGTCCTTCGTGCAGCAGATGAAATTTCTTGTAACACCTCTGCAGTTATCGGACGAGTTT | 20491 |
| | | | |
| QY | 428 | ATGCTGCAGACCCCTACACCAACACACTTGTCTCCAGCCCCCAAGCTACGGCGTTGGTGCA | 487 |
| | | | |
| Db | 2050 | ATGCTGCAGACCCCTACACCAAGCACTTGTCTCCAGCCCCCAAGCTACGGCGTTGGTGCA | 21099 |
| | | | |
| QY | 488 | TGANTGCTTTGGCCCTTGACCCATGTGCCAAGACTAGAGAGCCATGTCATATGTGGGTC | 547 |
| | | | |
| Db | 2110 | TGAATGCTTTGGACCTTTGACTGTGTGCCAAGACTAGAGAGCCATGTCATATGTGGGTC | 21699 |
| | | | |
| QY | 548 | TGCTTCTTTCTTCATTGAGGCTAGTATATACCAAGGGGGATACAAACCGTTTGTCTCAT | 607 |
| | | | |
| Db | 2170 | TGCTTCTTTCTTCATTGAGGCTAGTATATACCGAGGGGGATACAAACCGTTTGTCTCAT | 22229 |
| | | | |
| QY | 608 | A 608 | |
| | | | |
| Db | 2250 | A 2250 | |

```

3 RESULT 3
US-09-919-039-266
; Sequence 266. Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURE
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919, 039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 266
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO. US20030108871A1 253783.3
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1824
; OTHER INFORMATION: a, t, c, g, or other
US-09-919-039-266

```

| | Query Match | 13.0% | Score 79.4 | DB 11 | Length 1843 |
|----|---|----------------|-------------------|----------|-------------|
| | Best Local Similarity | 68.3% | Pred. No. 4.2e-16 | | |
| | Matches 110 | Conservative 0 | Mismatches 51 | Indels 0 | Gaps 0 |
| QY | 166 TCTGCATGCGCTTTCATATCCGGGCCCCACTGCTGCAGCTGCATACCGAGGGCT | 225 | | | |
| | | | | | |
| | | | | | |
| Db | 1312 TATGCAGTAGAGGGGGTTCCCTTACCACCCACCGGCAAGCGCTTGGCTTACGGGGGCGCA | 1371 | | | |
| QY | 226 CACCTTCGAGGCCCTGTGTGCGACCGGTGTACACACACTTTAGAGCTGGGGGGCCCCCACC | 285 | | | |
| | | | | | |
| | | | | | |
| Db | 1372 CATCTTCGGGGCGGGGGCGGGCGGTGTATATACATTTCCGGCTGGGCCACCCCAACC | 1431 | | | |
| | | | | | |
| | | | | | |

OY 286 CCAATCCCGCCTATGCGGAGTAGTGTATCAAGCCAGT 326
DB 1432 CCCATCCCGACTTACGAGGAGCGGAGTGGAGCAACGCTTGT 1472

RESULT 4

US-10-359-385-5
Sequence 5, Application US/10359385
Publication No. US20030143622A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Lu, Aina
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
FILE REFERENCE: PF-0611 US
CURRENT APPLICATION NUMBER: US/10/359,385
PRIOR FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/176,657
PRIOR FILING DATE: 1998-10-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PERL Program
SEQ ID NO 5
LENGTH: 1506
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: OTHER INFORMATION: 1250374
US-10-359-385-5

Query Match 10.4%; Score 63.2; DB 12; Length 1506;

Best Local Similarity 54.5%; Pred. No. 1,2e-10; Matches 279; Conservative 0; Mismatches 193; Indels 40; Gaps 6;

OY 1 ATGACTAATATAAGGCGCTGAACCCCTACACCAATGCTGGAATTAATCACTTGTG 60
DB 768 ATGACCAATAGAGAGATGCTACACCATATGCAAAATGTTGAAATTAAGCCAGTAGT 827
OY 61 GCGGGGCTTACAGCCCGGCTTATGAGGAGGAGCGTCTGT-----TGTCGAG 111
DB 828 GGAGCTGATATGATGCTCCGAGTATATGAGCATCGCTTCAAGCAGATGTGCTTA 887
OY 112 GCCAACGAGAGGATCTTCATGATGAGTGGCCCGGCTTCTATATCTGTGA 171
DB 888 GGCAATGATGAGAGTGGCTTATCAGAGAGAGGAGGATATCAACACTTACATCTTTA 947
OY 172 ---ATGCTGCTTTCATA---TCCGGCCGCGCTGCTGAGCTGATACCGAGGGCT 225
DB 948 ATCATTTCTGGCTTCCCTTACCTACTGACGACACGAGCGGCTTTAGAGAGGCG 1007
OY 226 CACCTTCGAGGCGGTGTGACCGGTGACCAACCTTACAGAGCTGGCGGCCCGCCACC 285
DB 1008 CATTTGAGGGGAGAGGGGCGAGAGTATGTGTGAGCTCGA---GCGGTACTCTCA 1064
OY 286 CCAATCCCGGCTATGCGGAGTATCAAGAGCGTATGCGCAATTAATGCGTA 345
DB 1065 GGCATCCCGGCTATTCAGAGGATGATATGACGCTTACAGATATGACAGCGCTGCT 1124
OY 346 CAGGTGTGTACGTCATACCGCTACGCGCCAGCCCGCTGCACTGCTGCTGCTAC 405
DB 1125 CAAC-----CGAGCGACCGGCTGCTGCGAGCGGCTTACCGGCTTAC 1165
OY 406 AGTGACAGTTACGAGAGATTATGCTGCCGACCCCTACACACACACTTCTCCAGCC 465
DB 1166 AGTGACAGTTATGAGGAGGCTGACAGCGAGCCCT---ACCATGCCCTTCCCTGCC 1222
OY 466 CCCACCTACGGGCTTGTGTCATGATGCTT 497
DB 1223 GCTACGTATGAGATGGCGCTGTGGCGAGTTT 1254

RESULT 5

US-09-908-975-7420
Sequence 7420, Application US/09908975
Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: MASSEMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Ilat
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLI
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7420
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-908-975-7420

Query Match 9.1%; Score 55.2; DB 12; Length 60;

Best Local Similarity 95.0%; Pred. No. 1.6e-08; Matches 57; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 499 GCGCCCTGACGAGTCCAGAGTACGAGCATGCTGATGATGAGTGGCTCGTCTTCT 558
DB 1 GCACCTTACTGATGATCCAGAGTACGAGCATGCTGATGATGAGTGGCTCGTCTTCT 60

RESULT 6

US-10-140-472-358/C
Sequence 358, Application US/10140472
Publication No. US20030138888A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C168
CURRENT APPLICATION NUMBER: US/10/140,472
PRIOR FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 2002-05-06
NUMBER OF SEQ ID NOS: 550
SOFTWARE: PatentIn version 3.0
SEQ ID NO 358
LENGTH: 1049
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-472-358

Query Match 6.0%; Score 36.8; DB 12; Length 1049;

Best Local Similarity 5.2%; Pred. No. 0.083;


```
RESULT 13
US-10-184-644-202/c
; Sequence 202, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C227
; CURRENT APPLICATION NUMBER: US/10/184,644
; PRIOR FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 202
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-644-202

Query Match
Best Local Similarity 15.9%; Score 35.4; DB 14; Length 440;
Matches 52; Conservative 88; Mismatches 188; Indels 0; Gaps 0;

OY 143 GCGCCAGTTCATCTTATATACCTTCGCAATGCGCTTCCATATCCGCGCCACCTG 202
DB 437 SST.HMN.THMN..C.MSM.NMW.AH.N.KC.SA.SBANBCCBTHCCSCGWSJC.CYRN 378
OY 203 CTCAGCTGCATACCGAGGGCTCACCCTTCGAGCGCGTGTGTCACCCGCTAGACACCT 262
DB 377 HCSGCC..YNC.MS..YKNSBSC.CY.C.CS.CSCYT.NC.M.GC.MDCNCCSCCDNCS 318
OY 263 TCAGAGCTGGCGGCCCCCAATCCCGGCTATGCGGAGTAGTATCAAGAGC 322
DB 317 SSCASSCWS.SCHYSCSNCSSCCSSCCSSSCSSSCSSSCNNHNCNSC 258
OY 323 CAGTGTATGSCAATAATGCTACAGGGTGTACGCTGATACCGCTAGCCGACGCCA 382
DB 257 SCSSCS..SCSCCSSNSSCCSSCS..NAGC.N.NSTYBSCRC..TBTC.AMAC.N..CCN 198
DB 383 CCCCTGCCACTGCTGCTGCTTACAGTAGACAGTACGAGCAGTTATGCTGCCGACCCCT 442
DB 197 CC.CW.TC..NKC.SCHSNC.RCDBW.AC.CC.NC.C.CC.CC.SC..CDCCSA.WTCSD 138
OY 443 ACCACACACACTGCTCCAGCCCCCAGC 470
DB 137 C.BC.WSCYBTHTCDY.BH.T.YC..DC 110

RESULT 14
US-10-184-634-202/c
; Sequence 202, Application US/10184634
; Publication No. US20030068684A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
```

```
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C217
; CURRENT APPLICATION NUMBER: US/10/184,634
; PRIOR FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 202
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-634-202

Query Match
Best Local Similarity 15.9%; Score 35.4; DB 14; Length 440;
Matches 52; Conservative 88; Mismatches 188; Indels 0; Gaps 0;

OY 143 GCGCCAGTTCATCTTATATACCTTCGCAATGCGCTTCCATATCCGCGCCACCTG 202
DB 437 SST.HMN.THMN..C.MSM.NMW.AH.N.KC.SA.SBANBCCBTHCCSCGWSJC.CYRN 378
OY 203 CTCAGCTGCATACCGAGGGCTCACCCTTCGAGCGCGTGTGTCACCCGCTAGACACCT 262
DB 377 HCSGCC..YNC.MS..YKNSBSC.CY.C.CS.CSCYT.NC.M.GC.MDCNCCSCCDNCS 318
OY 263 TCAGAGCTGGCGGCCCCCAATCCCGGCTATGCGGAGTAGTATCAAGAGC 322
DB 317 SSCASSCWS.SCHYSCSNCSSCCSSCCSSSCSSSCSSSCNNHNCNSC 258
OY 323 CAGTGTATGSCAATAATGCTACAGGGTGTACGCTGATACCGCTAGCCGACGCCA 382
DB 257 SCSSCS..SCSCCSSNSSCCSSCS..NAGC.N.NSTYBSCRC..TBTC.AMAC.N..CCN 198
OY 383 CCCCTGCCACTGCTGCTGCTTACAGTAGACAGTACGAGCAGTTATGCTGCCGACCCCT 442
DB 197 CC.CW.TC..NKC.SCHSNC.RCDBW.AC.CC.NC.C.CC.CC.SC..CDCCSA.WTCSD 138
OY 443 ACCACACACACTGCTCCAGCCCCCAGC 470
DB 137 C.BC.WSCYBTHTCDY.BH.T.YC..DC 110

RESULT 15
US-10-144-929-48
; Sequence 48, Application US/10144929
; Publication No. US20030069405A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2014P1
; CURRENT APPLICATION NUMBER: US/10/144,929
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US/09/251,329
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: PCT/US98/17044
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (393)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (401)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-144-929-48
```

| | | | | |
|---------------------------|--------|-----------------|-----------|-------------|
| Query Match | 5.88; | Score 35.4; | DB 14; | Length 660; |
| Best Local Similarity | 46.68; | Pred. No. 0.2; | | |
| Matches 102; Conservative | 3; | Mismatches 114; | Indels 0; | Gaps 0; |

OY AAGAGCCAGTGTATGGCACAATAATTGTCACAGGGGTGTACCTCGCATACGCCCTACGCC 376
||| ||| ||| ||| : ||| |||
Db AAGGAGAAGCAAGATGTGGACATGTTCGAAGAGGAGGCCAAGACTTGGAAGTCCAAGGCG 212
153
OY AGCCACACCCTGCACACTCTGCTGCCATACAGTAGACAGTTACGAGCAGATTATGCTGCCG 436
377
Db CTGGCAGGSCACAGCTCTGGCTGCTGACCGCTGAGAGCTGTCTGCGGGGCCCTGCTGGTCTGG 272
213
OY ACCCTTACCACACACACTTGTCTCAAGCCCCCACTACGGGCTTGGTGCATGATGCTT 496
437
Db ACCGTGGCTACGTGTAGCTGTGAACCCACACCTTTTCGAGGGGCTGTTGCCAMCCCTG 332
273
OY TTGCGCCCTTGACGATGCAGACATAGAGCGATGCTG 535
497
Db CTGAGCCCTGCACACCGTGTGGAAAGCTCCGGGCCCTGCTG 371
333

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job time : 186 secs

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OM nucleic - nucleic search, using sw model

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(Without alignments)
4977.821 Million cell updates/sec

Title: US-09-809-545a-1_COPY_535_1143

Perfect score: 609

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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 70 | 11.5 | 2372 | 3 | US-09-145-391-1 |
| 2 | 18 | 3.0 | 615 | 3 | US-09-286-284-29 |
| 3 | 18 | 3.0 | 664 | 3 | US-09-286-284-28 |
| 4 | 18 | 3.0 | 3364 | 4 | US-09-930-181-3 |
| 5 | 18 | 3.0 | 3431 | 4 | US-09-632-098-1 |
| 6 | 18 | 3.0 | 3468 | 4 | US-09-632-098-3 |
| 7 | 18* | 3.0 | 4830 | 3 | US-09-286-284-7 |
| 8 | 17 | 2.8 | 36 | 4 | US-09-337-307A-10 |
| 9 | 17 | 2.8 | 1757 | 1 | US-08-199-779-2 |
| 10 | 17 | 2.8 | 1757 | 1 | US-08-578-615A-105 |
| 11 | 17 | 2.8 | 1757 | 5 | PCT-US94-07770-105 |
| 12 | 17 | 2.8 | 1812 | 3 | US-08-199-779-1 |
| 13 | 17 | 2.8 | 1812 | 3 | US-08-578-615A-104 |
| 14 | 17 | 2.8 | 1812 | 5 | PCT-US94-07770-104 |
| 15 | 17 | 2.8 | 45546 | 4 | US-09-146-053-6 |
| 16 | 17 | 2.8 | 536165 | 4 | US-09-214-808-1 |
| 17 | 16 | 2.6 | 390 | 4 | US-09-328-352-2282 |
| 18 | 16 | 2.6 | 429 | 4 | US-09-252-991A-1762 |
| 19 | 16 | 2.6 | 437 | 1 | US-08-631-200-3 |
| 20 | 16 | 2.6 | 437 | 1 | US-08-631-200-4 |
| 21 | 16 | 2.6 | 437 | 1 | US-08-631-200-5 |
| 22 | 16 | 2.6 | 437 | 1 | US-08-829-553-3 |
| 23 | 16 | 2.6 | 437 | 1 | US-08-829-553-4 |
| 24 | 16 | 2.6 | 437 | 1 | US-08-829-553-5 |
| 25 | 16 | 2.6 | 437 | 2 | US-08-922-267A-3 |
| 26 | 16 | 2.6 | 437 | 2 | US-08-922-267A-4 |
| 27 | 16 | 2.6 | 437 | 2 | US-08-922-267A-5 |

| | | | | | | |
|----|----|-----|-----|---|---------------------|--------------------|
| 28 | 16 | 2.6 | 437 | 2 | US-08-936-707A-3 | Sequence 3, Appl1 |
| 29 | 16 | 2.6 | 437 | 2 | US-08-936-707A-4 | Sequence 4, Appl1 |
| 30 | 16 | 2.6 | 437 | 2 | US-08-936-707A-5 | Sequence 5, Appl1 |
| 31 | 16 | 2.6 | 437 | 2 | US-08-936-706A-3 | Sequence 3, Appl1 |
| 32 | 16 | 2.6 | 437 | 2 | US-08-936-706A-4 | Sequence 4, Appl1 |
| 33 | 16 | 2.6 | 437 | 2 | US-08-936-706A-5 | Sequence 5, Appl1 |
| 34 | 16 | 2.6 | 437 | 3 | US-09-248-203-3 | Sequence 3, Appl1 |
| 35 | 16 | 2.6 | 437 | 3 | US-09-248-203-4 | Sequence 4, Appl1 |
| 36 | 16 | 2.6 | 437 | 3 | US-09-248-203-5 | Sequence 5, Appl1 |
| 37 | 16 | 2.6 | 437 | 3 | US-09-406-071-3 | Sequence 3, Appl1 |
| 38 | 16 | 2.6 | 437 | 3 | US-09-406-071-4 | Sequence 4, Appl1 |
| 39 | 16 | 2.6 | 437 | 3 | US-09-406-071-5 | Sequence 5, Appl1 |
| 40 | 16 | 2.6 | 437 | 3 | US-08-905-223-86 | Sequence 86, Appl1 |
| 41 | 16 | 2.6 | 480 | 1 | US-08-630-592-5 | Sequence 5, Appl1 |
| 42 | 16 | 2.6 | 480 | 1 | US-08-714-991-5 | Sequence 5, Appl1 |
| 43 | 16 | 2.6 | 480 | 3 | US-09-032-165A-5 | Sequence 5, Appl1 |
| 44 | 16 | 2.6 | 833 | 2 | US-08-837-029-1 | Sequence 1, Appl1 |
| 45 | 16 | 2.6 | 918 | 4 | US-09-107-532A-2095 | Sequence 2095, Ap |

ALIGNMENTS

```
RESULT 1
US-09-145-391-1
: Sequence 1, Application US/09145391
: Patent No. 6194171
: GENERAL INFORMATION:
: APPLICANT: Puist, Stefan M.
: APPLICANT: Shibata, Hiroki
: TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
: TITLE OF INVENTION: Products Related Thereto and Methods of Using Same
: FILE REFERENCE: CE 3093
: CURRENT APPLICATION NUMBER: US/09/145,391
: CURRENT FILING DATE: 1998-09-01
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 1
: LENGTH: 2372
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (987)..(1979)
US-09-145-391-1

Query Match      11.5%; Score 70; DB 3; Length 2372;
Best Local Similarity 100.0%; Pred. No. 9,6e-27;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      511 GATGCCAAGACTGAGGACCATGCGATGATGATGGTCTGCTTCATTGACAGGCT 570
DB      2133 GATGCCAAGACTGAGGACCATGCTGATGATGGTCTGCTTCATTGACAGGCT 2192
QY      571 AGTATATACC 580
DB      2193 AGTATATACC 2202

RESULT 2
US-09-296-284-29
: Sequence 29, Application US/09296284A
: Patent No. 6204040
: GENERAL INFORMATION:
: APPLICANT: Choi, Eun-Sung
: APPLICANT: Rhee, Sang-Ri
: APPLICANT: Lee, Eun-Hae
: TITLE OF INVENTION: Glucobacter Suboxydans Sorbitol Dehydrogenase, Genes
: TITLE OF INVENTION: and Methods of Use Thereof
: FILE REFERENCE: 1533,0870000
: CURRENT APPLICATION NUMBER: US/09/296,284A
: CURRENT FILING DATE: 1999-04-22
: NUMBER OF SEQ ID NOS: 87
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
LENGTH: 615
TYPE: DNA
ORGANISM: Gluconobacter suboxydans
US-09-296-284-29

Query Match 3.0%; Score 18; DB 3; Length 615;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 GCGCCCCACCCCAATC 291
|||||
DB 48 GCGCCCCACCCCAATC 65

RESULT 3
US-09-296-284-28
Sequence 28, Application US/09296284A
Patent No. 6204040
GENERAL INFORMATION:
APPLICANT: Choi, Eun-Sung
APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae

TITLE OF INVENTION: Gluconobacter Suboxydans Sorbitol Dehydrogenase, Genes
TITLE OF INVENTION: and Methods of Use Thereof
FILE REFERENCE: 1533.0870000
CURRENT APPLICATION NUMBER: US/09/296,284A
CURRENT FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 28
LENGTH: 664
TYPE: DNA
ORGANISM: Gluconobacter suboxydans
US-09-296-284-28

Query Match 3.0%; Score 18; DB 3; Length 664;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 GCGCCCCACCCCAATC 291
|||||
DB 97 GCGCCCCACCCCAATC 114

RESULT 4
US-09-930-181-3/C
Sequence 3, Application US/09930181
Patent No. 6455292
GENERAL INFORMATION:
APPLICANT: Origene Technologies

TITLE OF INVENTION: Full-Length serine Protein Kinase In Brain and Pancreas
FILE REFERENCE: 160 101 VI
CURRENT APPLICATION NUMBER: US/09/930,181
CURRENT FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 3364
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (482)..(2239)
US-09-930-181-3

Query Match 3.0%; Score 18; DB 4; Length 3364;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 GCGGCGCCCAACCCCA 288
|||||

DB 3039 GCGGCGCCCAACCCCA 3022

RESULT 5
US-09-632-098-1
Sequence 1, Application US/09632098
Patent No. 6420154
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Balndur, Nand

APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
FILE REFERENCE: 99-39
CURRENT APPLICATION NUMBER: US/09/632,098
CURRENT FILING DATE: 2000-08-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 3431
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (37)...(2442)
US-09-632-098-1

Query Match 3.0%; Score 18; DB 4; Length 3431;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 GCGCCCAACCCCAATCC 293
|||||
DB 2978 GCGCCCAACCCCAATCC 2995

RESULT 6
US-09-632-098-3
Sequence 3, Application US/09632098
Patent No. 6420154
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.

APPLICANT: Balndur, Nand
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
FILE REFERENCE: 99-39
CURRENT APPLICATION NUMBER: US/09/632,098
CURRENT FILING DATE: 2000-08-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 3468
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (37)...(2472)
US-09-632-098-3

Query Match 3.0%; Score 18; DB 4; Length 3468;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 GCGCCCAACCCCAATCC 293
|||||
DB 3015 GCGCCCAACCCCAATCC 3032

RESULT 7
US-09-296-284-7
Sequence 7, Application US/09296284A
Patent No. 6204040
GENERAL INFORMATION:
APPLICANT: Choi, Eun-Sung

APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae
TITLE OF INVENTION: Gluconobacter Suboxydians Sorbitol Dehydrogenase. Genes
TITLE OF INVENTION: and Methods of use thereof
FILE REFERENCE: 1533.08/0000
CURRENT APPLICATION NUMBER: US/09/296.284A
CURRENT FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 4830
TYPE: DNA
ORGANISM: Gluconobacter suboxydians
US-09-296-284-7

Query Match 3.0%; Score 18; DB 3; Length 4830;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

274 GCGCCCCCACCCTCAATC 291
|||||
97 GCGCCCCCACCCTCAATC 114

RESULT 8
US-09-337-307A-10/c
Sequence 10, Application US/09337307A
Patent No. 6432692
GENERAL INFORMATION:
APPLICANT: Bradfield, Christopher A.
APPLICANT: Carver, Lucy A.
APPLICANT: Dunham, Elizabeth E.
TITLE OF INVENTION: Sensitive Biossay For Detecting Agonists Of The Aryl Hydrocarbon
FILE REFERENCE: WARP0105
CURRENT APPLICATION NUMBER: US/09/337.307A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 36
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-09-337-307A-10

Query Match 2.8%; Score 17; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

197 CCACTGCTGCAGCTGCA 213
|||||
30 CCACTGCTGCAGCTGCA 14

RESULT 9
US-08-199-779-2/c
Sequence 2, Application US/08199779
Patent No. 5681747
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonucleotide Modulation of
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: Kinase C
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & No. 5681747ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
MEDIUM TYPE: STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199.779
FILING DATE: herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 089,996
FILING DATE: July 9, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumond
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1757 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-199-779-2

Query Match 2.8%; Score 17; DB 1; Length 1757;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

277 CCCCCACCCCAATCCC 293
|||||
273 CCCCCACCCCAATCCC 257

RESULT 10
US-08-578-615A-105/c
Sequence 105, Application US/08578615A
Patent No. 6015892
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett and Russell, T. Boggs
TITLE OF INVENTION: Oligonucleotide Modulation of Protein Kinasec
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6015892ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578.615A
FILING DATE: 11-JAN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: 16-MAR-1992
APPLICATION NUMBER: 08/089,996
FILING DATE: 09-JUL-1993
APPLICATION NUMBER: 08/199,779
FILING DATE: 22-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Leggaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-1568
TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 1757 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-578-615A-105

Query Match 2.8%; Score 17; DB 3; Length 1757;
Best Local Similarity 100.0%; Pred. No. 31;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 CCCCCACCCCAATCCC 293
DB 273 CCCCCACCCCAATCCC 257

RESULT 11

Sequence 105, Application PC/RUS9407770

GENERAL INFORMATION:

APPLICANT: Nicholas Dean, C. Frank Bennett and
Applicant: Russell T. Boggs

TITLE OF INVENTION: Oligonucleotide Modulation of
NUMBER OF SEQUENCES: 119

Kinase C

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB

MEDIUM TYPE: STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/07770

FILING DATE: herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 852,852

FILING DATE: March 16, 1992

APPLICATION NUMBER: 08/089,996

FILING DATE: July 9, 1993

APPLICATION NUMBER: 08/199,779

FILING DATE: February 22, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Rebecca Ralph Gaumond

REGISTRATION NUMBER: 35,152

REFERENCE/DOCKET NUMBER: ISIS-1546

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:

LENGTH: 1757 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

PCT-US94-07770-105

Query Match 2.8%; Score 17; DB 5; Length 1757;
Best Local Similarity 100.0%; Pred. No. 31;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 CCCCCACCCCAATCCC 293
DB 273 CCCCCACCCCAATCCC 257

RESULT 12

US-08-199-779-1/C

Sequence 1, Application US/08199779

Patent No. 5681747

GENERAL INFORMATION:

APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonucleotide Modulation of
NUMBER OF SEQUENCES: 17

Kinase C

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB

MEDIUM TYPE: STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/199,779

FILING DATE: herewith

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 089,996

FILING DATE: July 9, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Rebecca Ralph Gaumond

REGISTRATION NUMBER: 35,152

REFERENCE/DOCKET NUMBER: ISIS-1242

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1812 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-199-779-1

Query Match 2.8%; Score 17; DB 1; Length 1812;
Best Local Similarity 100.0%; Pred. No. 31;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 CCCCCACCCCAATCCC 293
DB 328 CCCCCACCCCAATCCC 312

RESULT 13

US-08-578-615A-104/C

Sequence 104, Application US/08578615A

Patent No. 6015892

GENERAL INFORMATION:

APPLICANT: Nicholas Dean, C. Frank Bennett and Russell, T. Boggs

TITLE OF INVENTION: Oligonucleotide Modulation of Protein Kinase

NUMBER OF SEQUENCES: 122

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6015892r1s LLP

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,615A
FILING DATE: 11-JAN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: 16-MAR-1992
APPLICATION NUMBER: 08/089,996
FILING DATE: 09-JUL-1993
APPLICATION NUMBER: 08/199,779
FILING DATE: 22-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-1568
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEO ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 1812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-578-615A-104

Query Match 2.88; Score 17; DB 3; Length 1612;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 CCCCCACCCCAATCCC 293
DB 328 CCCCCACCCCAATCCC 312

RESULT 14
PCT-US94-07770-104/C
Sequence 104, Application PC/TUS9407770
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett and
APPLICANT: Russell T. Boggs
TITLE OF INVENTION: Oligonucleotide Modulation of
TITLE OF INVENTION: Protein Kinase C
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: MacKiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
MEDIUM TYPE: STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07770
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852

FILING DATE: March 16, 1992
APPLICATION NUMBER: 08/089,996
FILING DATE: July 9, 1993
APPLICATION NUMBER: 08/199,779
FILING DATE: February 22, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumond
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEO ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 1812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US94-07770-104

Query Match 2.88; Score 17; DB 5; Length 1812;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 277 CCCCCACCCCAATCCC 293
DB 328 CCCCCACCCCAATCCC 312

RESULT 15
US-09-146-053-6
Sequence 6, Application US/09146053A
Patent No. 6399349
GENERAL INFORMATION:
APPLICANT: Ryan, James W.
APPLICANT: Sprinkle, Terry Joe Curtis
APPLICANT: Venema, Richard C.
TITLE OF INVENTION: Human Aminopeptidase P Gene
FILE REFERENCE: MCG103
CURRENT APPLICATION NUMBER: US/09/146,053A
CURRENT FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/057,854
EARLIER FILING DATE: 1997-09-02
NUMBER OF SEO ID NOS: 7
SOFTWARE: Patentln Ver. 2.0
SEO ID NO 6
LENGTH: 45546
TYPE: DNA
ORGANISM: Homo sapiens
US-09-146-053-6

Query Match 2.88; Score 17; DB 4; Length 45546;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 ACCGCTACGCCAGCCC 381
DB 22991 ACCGCTACGCCAGCCC 23007

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Job time : 55 secs

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OM nucleic - nucleic search, using sw model

Run on: September 25, 2003, 11:03:44 : Search time 54 Seconds
(without alignments)
4896.083 million cell updates/sec

Title: US-09-809-545A-1_COPY_545_1143

Perfect score: 599
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

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6: /cgn2_6/ptodata/1/lna/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 70 | 11.7 | 2372 | 3 | US-09-145-391-1 |
| 2 | 18 | 3.0 | 615 | 3 | US-09-296-284-29 |
| 3 | 18 | 3.0 | 664 | 3 | US-09-296-284-28 |
| 4 | 18 | 3.0 | 3364 | 4 | US-09-930-181-3 |
| 5 | 18 | 3.0 | 3431 | 4 | US-09-632-098-1 |
| 6 | 18 | 3.0 | 3468 | 4 | US-09-632-098-3 |
| 7 | 18 | 3.0 | 4830 | 4 | US-09-296-284-7 |
| 8 | 17 | 2.8 | 36 | 4 | US-09-337-307A-10 |
| 9 | 17 | 2.8 | 1757 | 1 | US-08-199-779-2 |
| 10 | 17 | 2.8 | 1757 | 1 | US-08-578-615A-105 |
| 11 | 17 | 2.8 | 1757 | 5 | PCT-US94-07770-105 |
| 12 | 17 | 2.8 | 1812 | 1 | US-08-199-779-1 |
| 13 | 17 | 2.8 | 1812 | 3 | US-08-578-615A-104 |
| 14 | 17 | 2.8 | 1812 | 5 | PCT-US94-07770-104 |
| 15 | 17 | 2.8 | 45546 | 4 | US-09-146-053-6 |
| 16 | 17 | 2.8 | 536165 | 4 | US-09-214-808-1 |
| 17 | 16 | 2.7 | 390 | 4 | US-09-328-352-2282 |
| 18 | 16 | 2.7 | 429 | 4 | US-09-252-991A-1762 |
| 19 | 16 | 2.7 | 437 | 1 | US-08-631-200-3 |
| 20 | 16 | 2.7 | 437 | 1 | US-08-631-200-4 |
| 21 | 16 | 2.7 | 437 | 1 | US-08-631-200-5 |
| 22 | 16 | 2.7 | 437 | 1 | US-08-829-553-3 |
| 23 | 16 | 2.7 | 437 | 1 | US-08-829-553-4 |
| 24 | 16 | 2.7 | 437 | 1 | US-08-829-553-5 |
| 25 | 16 | 2.7 | 437 | 2 | US-08-922-267A-3 |
| 26 | 16 | 2.7 | 437 | 2 | US-08-922-267A-4 |
| 27 | 16 | 2.7 | 437 | 2 | US-08-922-267A-5 |

| | | | | | | |
|----|----|-----|-----|---|---------------------|--------------------|
| 28 | 16 | 2.7 | 437 | 2 | US-08-936-707A-3 | Sequence 3, Appli |
| 29 | 16 | 2.7 | 437 | 2 | US-08-936-707A-4 | Sequence 4, Appli |
| 30 | 16 | 2.7 | 437 | 2 | US-08-936-707A-5 | Sequence 5, Appli |
| 31 | 16 | 2.7 | 437 | 2 | US-08-936-706A-3 | Sequence 3, Appli |
| 32 | 16 | 2.7 | 437 | 2 | US-08-936-706A-4 | Sequence 4, Appli |
| 33 | 16 | 2.7 | 437 | 2 | US-08-936-706A-5 | Sequence 5, Appli |
| 34 | 16 | 2.7 | 437 | 3 | US-09-248-203-3 | Sequence 3, Appli |
| 35 | 16 | 2.7 | 437 | 3 | US-09-248-203-4 | Sequence 4, Appli |
| 36 | 16 | 2.7 | 437 | 3 | US-09-248-203-5 | Sequence 5, Appli |
| 37 | 16 | 2.7 | 437 | 3 | US-09-406-071-3 | Sequence 3, Appli |
| 38 | 16 | 2.7 | 437 | 3 | US-09-406-071-4 | Sequence 4, Appli |
| 39 | 16 | 2.7 | 437 | 3 | US-09-406-071-5 | Sequence 5, Appli |
| 40 | 16 | 2.7 | 437 | 3 | US-08-905-223-86 | Sequence 86, Appli |
| 41 | 16 | 2.7 | 480 | 1 | US-08-630-592-5 | Sequence 5, Appli |
| 42 | 16 | 2.7 | 480 | 1 | US-08-714-991-5 | Sequence 5, Appli |
| 43 | 16 | 2.7 | 480 | 3 | US-09-032-365A-5 | Sequence 5, Appli |
| 44 | 16 | 2.7 | 833 | 2 | US-08-837-029-1 | Sequence 1, Appli |
| 45 | 16 | 2.7 | 918 | 4 | US-09-107-532A-2095 | Sequence 2095, Ap |

ALIGNMENTS

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RESULT 1
US-09-145-391-1
: Sequence 1, Application US/09145391
: Patent No. 6194171
: GENERAL INFORMATION:
: APPLICANT: Pulist, Stefan M.
: TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
: TITLE OF INVENTION: Products Related Thereto and Methods of Using Same
: FILE REFERENCE: CE 3093
: CURRENT APPLICATION NUMBER: US/09/145,391
: CURRENT FILING DATE: 1998-09-01
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 1
: LENGTH: 2372
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (987)..(1979)
US-09-145-391-1

Query Match          11.7%; Score 70; DB 3; Length 2372;
Best Local Similarity 100.0%; Pred. No. 6.2e-27;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 501 GATCCCAAGACTAGAGCCATGTCGATGATGTCGTCCTTCATTCAGAGCT 560
DB 2133 GATCCCAAGACTAGAGCCATGTCGATGATGTCGTCCTTCATTCAGAGCT 2192
QY 561 AGTATATACC 570
DB 2193 AGTATATACC 2202

RESULT 2
US-09-296-284-29
: Sequence 29, Application US/09296284A
: Patent No. 6204040
: GENERAL INFORMATION:
: APPLICANT: Choi, Eun-Sung
: APPLICANT: Rhee, Sang-Ki
: APPLICANT: Lee, Eun-Hae
: TITLE OF INVENTION: Glucosyltransferase Suboxylans Sorbitol Dehydrogenase, Genes
: TITLE OF INVENTION: and Methods of Use Thereof
: FILE REFERENCE: 1533.0870000
: CURRENT APPLICATION NUMBER: US/09/296,284A
: CURRENT FILING DATE: 1999-04-22
: NUMBER OF SEQ ID NOS: 87
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SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Gluconobacter suboxydans
US-09-296-284-29

Query Match 3.0%; Score 18; DB 3; Length 615;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 264 GCGCCCCCACCACCAATC 281
DB 48 GCGCCCCCACCACCAATC 65

RESULT 3
US-09-296-284-28
; Sequence 28, Application US/09296284A
Patent No. 6204040

GENERAL INFORMATION:
; APPLICANT: Choi, Eun-Sung
; APPLICANT: Rhee, Sang-Ki
; APPLICANT: Lee, Eun-Hae
; TITLE OF INVENTION: Gluconobacter Suboxydans Sorbitol Dehydrogenase, Genes
; FILE REFERENCE: 1533.0870000
; CURRENT APPLICATION NUMBER: US/09/296,284A
; CURRENT FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 664
; TYPE: DNA
; ORGANISM: Gluconobacter suboxydans
US-09-296-284-28

Query Match 3.0%; Score 18; DB 3; Length 664;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 264 GCGCCCCCACCACCAATC 281
DB 97 GCGCCCCCACCACCAATC 114

RESULT 4
US-09-930-181-3/C

Sequence 3, Application US/09930181
Patent No. 6455292

GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 V1
; CURRENT APPLICATION NUMBER: US/09/930,181
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 3364
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (482)..(2239)
US-09-930-181-3

Query Match 3.0%; Score 18; DB 4; Length 3364;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 261 GCGCGCCCCCACCACCA 278
DB 11111111111111111111

DB 3039 GCGCGCCCCCACCACCA 3022

RESULT 5

US-09-632-098-1
; Sequence 1, Application US/09632098
Patent No. 6420154

GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Balndur, Nand
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
; FILE REFERENCE: 99-39
; CURRENT APPLICATION NUMBER: US/09/632,098
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows version 3.0
; SEQ ID NO 1
; LENGTH: 3431
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (37)...(2442)
US-09-632-098-1

Query Match 3.0%; Score 18; DB 4; Length 3431;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 266 GCGCGCCCCCACCACCAATCC 283
DB 2978 GCGCGCCCCCACCACCAATCC 2995

RESULT 6

US-09-632-098-3
; Sequence 3, Application US/09632098
Patent No. 6420154

GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Balndur, Nand
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
; FILE REFERENCE: 99-39
; CURRENT APPLICATION NUMBER: US/09/632,098
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows version 3.0
; SEQ ID NO 3
; LENGTH: 3468
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (37)...(2472)
US-09-632-098-3

Query Match 3.0%; Score 18; DB 4; Length 3468;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 266 GCGCGCCCCCACCACCAATCCC 283
DB 3015 GCGCGCCCCCACCACCAATCCC 3032

RESULT 7

US-09-296-284-7

Sequence 7, Application US/09296284A
Patent No. 6204040
GENERAL INFORMATION:
; APPLICANT: Choi, Eun-Sung

APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae
TITLE OF INVENTION: Glucobacter Suboxydans Sorbitol Dehydrogenase. Genes
FILE REFERENCE: 1533.08/0000
CURRENT APPLICATION NUMBER: US/09/296,284A
CURRENT FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 4830
TYPE: DNA
ORGANISM: Gluconobacter suboxydans
US-09-296-284-7

Query Match 3.08; Score 18; DB 3; Length 4830;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

264 GCGCCCCCACCACATC 281
|||||
97 GCGCCCCCACCACATC 114

RESULT 8
US-09-337-307A-10/c
Sequence 10, Application US/09337307A
Patent No. 6432692
GENERAL INFORMATION:
APPLICANT: Bradford, Christopher A.
APPLICANT: Carver, Lucy A.
APPLICANT: Dunham, Elizabeth E.
TITLE OF INVENTION: Sensitive Biosay For Detecting Agonists Of The Aryl Hydrocarbon
FILE REFERENCE: MARP0105
CURRENT APPLICATION NUMBER: US/09/337,307A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 36
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-09-337-307A-10

Query Match 2.88; Score 17; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

187 CCACTGCTGCAGCTGCA 203
|||||
30 CCACTGCTGCAGCTGCA 14

RESULT 9
US-08-199-779-2/c
Sequence 2, Application US/08199779
Patent No. 5681747
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonucleotide Modulation of Kinase C
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & No. 5681747ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
MEDIUM TYPE: STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,779
FILING DATE: herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 089,996
FILING DATE: July 9, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumond
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1757 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-199-779-2

Query Match 2.88; Score 17; DB 1; Length 1757;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

267 CCCCCCCCCCAATCC 283
|||||
273 CCCCCCCCCCAATCC 257

RESULT 10
US-08-578-615A-105/c
Sequence 105, Application US/08578615A
Patent No. 6013892
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett and Russell, T. Boggs
TITLE OF INVENTION: Oligonucleotide Modulation of Protein Kinase C
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6015892ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,615A
FILING DATE: 11-JAN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: 16-MAR-1992
APPLICATION NUMBER: 08/089,996
FILING DATE: 09-JUL-1993
APPLICATION NUMBER: 08/199,779
FILING DATE: 22-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Leggaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-1568
TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 1757 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-578-615A-105

Query Match 2.8%; Score 17; DB 3; Length 1757;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 267 CCCCCCCCCCAATCCC 283
DB 273 CCCCCCCCCCAATCCC 257

SUPL 11
T-US94-07770-105/C
Sequence 105, Application PC/TUS9407770
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett and
APPLICANT: Russell T. Boggs
TITLE OF INVENTION: Oligonucleotide Modulation of
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

Kinase C

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
MEDIUM TYPE: STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07770
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: March 16, 1992
APPLICATION NUMBER: 08/089,996
FILING DATE: July 9, 1993
APPLICATION NUMBER: 08/199,779
FILING DATE: February 22, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumond
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 1757 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US94-07770-105

Query Match 2.8%; Score 17; DB 5; Length 1757;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 267 CCCCCCCCCCAATCCC 283
DB 273 CCCCCCCCCCAATCCC 257

RESULT 12
US-08-199-779-1/C
Sequence 1, Application US/08199779
Patent No. 5681747
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonucleotide Modulation of
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & No. 5681747ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

Kinase C

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
MEDIUM TYPE: STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,779
FILING DATE: herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 089,996
FILING DATE: July 9, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumond
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-199-779-1

Query Match 2.8%; Score 17; DB 1; Length 1812;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 267 CCCCCCCCCCAATCCC 283
DB 328 CCCCCCCCCCAATCCC 312

RESULT 13
US-08-578-615A-104/C
Sequence 104, Application US/08578615A
Patent No. 6015892
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett and Russell, T. Boggs
TITLE OF INVENTION: Oligonucleotide Modulation of Protein Kinase C
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6015892ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia

STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,615A
FILING DATE: 11-JAN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: 16-MAR-1992
APPLICATION NUMBER: 08/089,996
FILING DATE: 09-JUL-1993
APPLICATION NUMBER: 08/199,779
FILING DATE: 22-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-1568
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 1812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-578-615A-104

Query Match 2.8%; Score 17; DB 3; Length 1812;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 267 CCCCACCCCAATCCC 283
DB 328 CCCCACCCCAATCCC 312

RESULT 14
PCT-US94-07770-104/C
Sequence 104, Application PC/TUS9407770
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett and
APPLICANT: Russell T. Boggs
TITLE OF INVENTION: Oligonucleotide Modulation of
KINASE C
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
MEDIUM TYPE: STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07770
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852

FILING DATE: March 16, 1992
APPLICATION NUMBER: 08/089,996
FILING DATE: July 9, 1993
APPLICATION NUMBER: 08/199,779
FILING DATE: February 22, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumond
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 1812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US94-07770-104

Query Match 2.8%; Score 17; DB 5; Length 1812;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 267 CCCCACCCCAATCCC 283
DB 328 CCCCACCCCAATCCC 312

RESULT 15
US-09-146-053-6
Sequence 6, Application US/09146053A
Patent No. 639349
GENERAL INFORMATION:
APPLICANT: Ryan, James W.
APPLICANT: Sprinkle, Terry Joe Curtis
APPLICANT: Venema, Richard C.
TITLE OF INVENTION: Human Antinopeptidase P Gene
FILE REFERENCE: MCG103
CURRENT APPLICATION NUMBER: US/09/146,053A
CURRENT FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/057,854
EARLIER FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 45546
TYPE: DNA
ORGANISM: Homo sapiens
US-09-146-053-6

Query Match 2.8%; Score 17; DB 4; Length 45546;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 ACCGCTACGCCAGCCC 371
DB 22991 ACCGCTACGCCAGCCC 23007

Search completed: September 25, 2003, 11:47:52
Job time : 55 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 25, 2003, 11:37:54 ; Search time 166 Seconds
(without alignments)
8983.163 Million cell updates/sec

Title: US-09-809-545A-1_COPY_545_1143
Perfect score: 599
Sequence: 1 aaaaagccgtgaaccctac.....acaacgcttgctccatcat 599

Scoring table:
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Gapop 60.0 , Gapext 60.0

Searched: 1678620 seqs, 1244745471 residues

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Total number of hits satisfying chosen parameters: 3357240

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpna/PCF_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCFUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 599 | 100.0 | 1340 | 10 | US-09-809-545A-1 |
| 2 | 70 | 11.7 | 2372 | 9 | US-09-794-591-1 |
| 3 | 48 | 8.0 | 60 | 12 | US-09-908-975-7420 |
| 4 | 21 | 3.5 | 713 | 21 | US-10-027-632-26954 |
| 5 | 20 | 3.3 | 414 | 11 | US-10-027-632-150999 |
| 6 | 20 | 3.3 | 414 | 11 | US-09-918-995-9070 |
| 7 | 20 | 3.3 | 4684 | 14 | US-10-205-823-106 |
| 8 | 18 | 3.0 | 278 | 10 | US-09-783-590-7497 |
| 9 | 18 | 3.0 | 332 | 10 | US-09-969-708-535 |
| 10 | 18 | 3.0 | 458 | 11 | US-09-918-995-565 |
| 11 | 18 | 3.0 | 472 | 11 | US-09-918-995-381 |
| 12 | 18 | 3.0 | 472 | 11 | US-09-918-995-25844 |
| 13 | 18 | 3.0 | 559 | 13 | US-10-027-632-193231 |
| 14 | 18 | 3.0 | 559 | 13 | US-10-027-632-193232 |
| 15 | 18 | 3.0 | 586 | 13 | US-10-027-632-131089 |
| 16 | 18 | 3.0 | 620 | 13 | US-10-027-632-14363 |

| | | | | | | |
|----|----|-----|------|----|----------------------|-------------------|
| 17 | 18 | 3.0 | 650 | 13 | US-10-027-632-22344 | Sequence 22244, |
| 18 | 18 | 3.0 | 2173 | 14 | US-10-102-558-1 | Sequence 1, App11 |
| 19 | 18 | 3.0 | 2407 | 13 | US-10-027-632-101774 | Sequence 101774, |
| 20 | 18 | 3.0 | 2830 | 12 | US-10-267-459-1 | Sequence 1, |
| 21 | 18 | 3.0 | 2830 | 12 | US-10-209-059-5 | Sequence 1, App11 |
| 22 | 18 | 3.0 | 3364 | 14 | US-10-195-072-3 | Sequence 3, App11 |
| 23 | 18 | 3.0 | 3364 | 14 | US-10-195-071-3 | Sequence 3, App11 |
| 24 | 18 | 3.0 | 3431 | 12 | US-10-177-308-1 | Sequence 1, App11 |
| 25 | 18 | 3.0 | 3468 | 12 | US-10-177-308-3 | Sequence 3, App11 |
| 26 | 18 | 3.0 | 3582 | 12 | US-10-199-672-465 | Sequence 465, |
| 27 | 18 | 3.0 | 3582 | 12 | US-10-187-749-465 | Sequence 465, |
| 28 | 18 | 3.0 | 3582 | 12 | US-10-194-457-465 | Sequence 465, |
| 29 | 18 | 3.0 | 3582 | 12 | US-10-184-642-465 | Sequence 465, |
| 30 | 18 | 3.0 | 3582 | 12 | US-10-196-747-465 | Sequence 465, |
| 31 | 18 | 3.0 | 3582 | 12 | US-10-173-689-465 | Sequence 465, |
| 32 | 18 | 3.0 | 3582 | 12 | US-10-173-691-465 | Sequence 465, |
| 33 | 18 | 3.0 | 3582 | 12 | US-10-173-691-465 | Sequence 465, |
| 34 | 18 | 3.0 | 3582 | 12 | US-10-173-692-465 | Sequence 465, |
| 35 | 18 | 3.0 | 3582 | 12 | US-10-173-694-465 | Sequence 465, |
| 36 | 18 | 3.0 | 3582 | 12 | US-10-173-698-465 | Sequence 465, |
| 37 | 18 | 3.0 | 3582 | 12 | US-10-173-699-465 | Sequence 465, |
| 38 | 18 | 3.0 | 3582 | 12 | US-10-173-707-465 | Sequence 465, |
| 39 | 18 | 3.0 | 3582 | 12 | US-10-174-569-465 | Sequence 465, |
| 40 | 18 | 3.0 | 3582 | 12 | US-10-174-583-465 | Sequence 465, |
| 41 | 18 | 3.0 | 3582 | 12 | US-10-174-587-465 | Sequence 465, |
| 42 | 18 | 3.0 | 3582 | 12 | US-10-174-589-465 | Sequence 465, |
| 43 | 18 | 3.0 | 3582 | 12 | US-10-174-591-465 | Sequence 465, |
| 44 | 18 | 3.0 | 3582 | 12 | US-10-175-336-465 | Sequence 465, |
| 45 | 18 | 3.0 | 3582 | 12 | US-10-175-742-465 | Sequence 465, |

ALIGNMENTS

RESULT 1
US-09-809-545A-1
Sequence 1, Application US/09809545A
Patent No. US20020110804A1
GENERAL INFORMATION:
APPLICANT: Staton, Lawrence W.
APPLICANT: White, R. Tyler
TITLE OF INVENTION: SECRETED FACTORS
FILE REFERENCE: SCIOS.017A
CURRENT APPLICATION NUMBER: US/09/809, 545A
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1340
TYPE: DNA
ORGANISM: Rattus norvegicus
US-09-809-545A-1

Query Match 100.0%; Score 599; DB 10; Length 1340;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 1 | AAAAGCGCGTGAACCCCTACACCAATGGCTGGAATTAATCCAGTTGTGGCCGGTCT | 60 |
| DB | 545 | AAAAGCGCGTGAACCCCTACACCAATGGCTGGAATTAATCCAGTTGTGGCCGGTCT | 604 |
| QY | 61 | ACAGCCCGCACTTATGACGACGAGTGTGTCGACAGCCAGAGGAGATCTT | 120 |
| DB | 605 | ACAGCCCGCACTTATGACGACGAGTGTGTCGACAGCCAGAGGAGATCTT | 664 |
| QY | 121 | CCATGTACAGTGGCCCGAGTTCACTTGTATATACCTTGCATAGCCGTGGCTTCATATC | 180 |
| DB | 665 | CCATGTACAGTGGCCCGAGTTCACTTGTATATACCTTGCATAGCCGTGGCTTCATATC | 724 |
| QY | 181 | CGGCGCCACTGTCGACGTCGATACCGAGGGGCTACCTTCGAGCGCGTGCACCG | 240 |
| DB | 725 | CGGCGCCACTGTCGACGTCGATACCGAGGGGCTACCTTCGAGCGCGTGCACCG | 784 |

| | | | |
|----|------|---|------|
| OY | 241 | TGTACAAACACCTTCAGAGCTGGGGGGCCCCCAACCCCAATGCGGCTATGGCGAGTAG | 300 |
| Db | 785 | TGTACAAACACTTCAGAGCTGGGGGGCCCCCAACCCCAATGCGGCTATGGCGAGTAG | 844 |
| OY | 301 | TGTATCAAGAGCCACTGTATGGCAATAATTCTACAGGGTGTTACGCTGCATACCGCT | 360 |
| Db | 845 | TGTATCAAGAGCCACTGTATGGCAATAATTCTACAGGGTGTTACGCTGCATACCGCT | 904 |
| OY | 361 | ACGCCAGACCCACCCCTGCCTACACTGTGGTGCCTACAGACGATTACGAGACAGATTATG | 420 |
| Db | 905 | ACGCCAGACCCACCCCTGCCTACACTGTGGTGCCTACAGACGATTACGAGACAGATTATG | 964 |
| OY | 421 | CTGGCCGACCCCTACCAACACACACACTGCTCCAGCCCCCAACGCTACGGCGTTGGTGCATGA | 480 |
| Db | 965 | CTGGCCGACCCCTACCAACACACACACTGCTCCAGCCCCCAACGCTACGGCGTTGGTGCATGA | 1024 |
| OY | 481 | ATGCTTTTGGCCCTTGGACGATGCCAAGACTAGAGACGATGCTGATGATGGGGTCTCG | 540 |
| Db | 1025 | ATGCTTTTGGCCCTTGGACGATGCCAAGACTAGAGACGATGCTGATGATGGGGTCTCG | 1088 |
| OY | 541 | TTCTTTCTTCACATGACGCTAGTATATATACCAAGGGGGATACACCGCTTTTGGTCCATAT | 599 |
| Db | 1085 | TTCTTTCTTCACATGACGCTAGTATATATACCAAGGGGGATACACCGCTTTTGGTCCATAT | 1143 |

```

RESULT 2
US-09-794-591-1
: Sequence 1, Application US/09794591
: Patent No. US20010018198A1
: GENERAL INFORMATION:
: APPLICANT: Pulst, Stefan M.
: APPLICANT: Shbate, Hiroki
: TITLE OF INVENTION: Nucleic Acids Encoded Thereeto and Methods of Using Same
: FILE REFERENCE: CE 3093
: CURRENT APPLICATION NUMBER: US/09/794,591
: PRIOR APPLICATION NUMBER: 2001-02-26
: PRIOR FILING DATE: 1998-09-01
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 2372
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (987)..(1979)
-09-794-591-1

Query Match      11.7%; Score 70; DB 9; Length 2372;
Best Local Similarity 100.0%; Pred. No. 8,4e-28;
Matches 70; Conservative 0; Mismatches 0; Gaps 0; Models 0;

OY      501 GATGCCAAGACTAGAGCCATGCTGATGATGATGTGGGCTCTGTCCTTCTTCATTTGAGGCT 560
      |||||||
Db      2133 GATGCCCAAGACTAGAGCCATGCTGATGATGATGTGGGCTCTGTCCTTCTTCATTTGAGGCT 2192

OY      561 AGTATATACC 570
      |||||||
Db      2193 AGTATATACC 2202

RESULT 3
US-09-908-975-7420
: Sequence 7420, Application US/09908975
: Publication No. US20030165843A1
: GENERAL INFORMATION:
: APPLICANT: SHOSHAN, AVI
: APPLICANT: MASSEMAN, ALON
: APPLICANT: MINTZ, ELLI
: APPLICANT: MINTZ, LIAT
: APPLICANT: FAIGLER, SIMCHON

```

```

? TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPL
? TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
? FILE REFERENCE: 36686-0005
? CURRENT APPLICATION NUMBER: US/09/908,975
? CURRENT FILING DATE: 2001-07-20
? PRIOR APPLICATION NUMBER: US 60/287,724
? PRIOR FILING DATE: 2001-05-02
? PRIOR APPLICATION NUMBER: US 60/221,607
? PRIOR FILING DATE: 2000-07-28
? NUMBER OF SEQ ID NOS: 32337
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 7420
? LENGTH: 60
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-908-975-7420

Query Match      8.0%; Score 48; DB 12; Length 60;
Best Local Similarity 100.0%; Pred. No. 9.2e-16;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      501 GATGCCAAGACTAGAGGACCATGCTGATGATGTGGGCTCGTTCTTTCT 548
        |||||||
Db      13 GATGCCAAGACTAGAGGACCATGCTGATGATGTGGGCTCTGTTCTTTCT 60

```

```

RESULT 4
US-10-027-632-26954/C
; Sequence 26954, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26954
; LENGTH: 713
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-26954

Query Match          3.5%; Score 21; DB 13; Length 713;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      32 GAATTAATCCAGTGTGGG 52
        |||
Db      231 GAATTAATCCAGTGTGGG 211

RESULT 5
US-10-027-632-150999/C
; Sequence 150999, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

```

```

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218, 006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198, 676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193, 483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185, 218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167, 363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156, 358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146, 002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150999
; LENGTH: 713
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-150999

```

```

Query Match          3.5%; Score 21; DB 13; Length 713;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      32 GAATTAATCACTGTGTGG 52
      |||||||
Db      231 GAATTAATCACTGTGTGG 211

```

```

RESULT 6
US-09-918-995-9070
; Sequence 9070, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918, 995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235, 076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9070
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(414)
; OTHER INFORMATION: n - A,T,C or G
US-09-918-995-9070

```

```

Query Match          3.3%; Score 20; DB 11; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      144 CTGTATATACCTTCTGCAAT 163
      |||||||
Db      180 CTGTATATACCTTCTGCAAT 199

```

```

RESULT 7
US-10-205-823-106
; Sequence 106, Application US/10205823
; Publication No. US20030108963A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glat, Karen
; APPLICANT: Zhao, Xumei
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205, 823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307, 982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314, 356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325, 020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341, 746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362, 158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 4684
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-205-823-106

```

```

Query Match          3.3%; Score 20; DB 14; Length 4684;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      144 CTGTATATACCTTCTGCAAT 163
      |||||||
Db      3962 CTGTATATACCTTCTGCAAT 3981

```

```

RESULT 8
US-09-783-590-7497
; Sequence 7497, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16, 2C1
; CURRENT APPLICATION NUMBER: US/09/783, 590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420, 856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346, 731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 7497
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (31)
; OTHER INFORMATION: n equals a,t,g, or c

```

```

? NAME/KEY: misc feature
? LOCATION: (137)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (161)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (165)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (172)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (252)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (266)
? OTHER INFORMATION: n equals a,t,g, or c
? NAME/KEY: misc feature
? LOCATION: (271)
? OTHER INFORMATION: n equals a,t,g, or c

```

| | | | | |
|-----------------------|-----------------|---------------|-----------|-------------|
| Query Match | 3.0% | Score 18; | DB 10; | Length 278; |
| Best Local Similarity | 100.0% | Pred. NO. 22; | | |
| Matches 18; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0 |

| | | | |
|----|-----|-------------------|-----|
| Qy | 266 | GGCCCGACCCCAATCCC | 283 |
| | | | |
| Db | 115 | GGCCCGACCCCAATCCC | 132 |

RESULT 9
US-09-969-708-535/c
; Sequence 535, Application US/09969708
; Patent No. US20020102532a1

```

: TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
: TITLE OF INVENTION: Sets
: FILE REFERENCE: 689290-70
: CURRENT APPLICATION NUMBER: US/09/969,708
: CURRENT FILING DATE: 2001-10-03
: PRIOR APPLICATION NUMBER: US/60/237,606
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: US/60/237,608
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: US/60/237,425
: PRIOR FILING DATE: 2000-10-03
: NUMBER OF SEQ ID NOS: 658
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 535
: LENGTH: 332
: TYPE: DNA
: ORGANISM: Homosapiens
: FEATURE:
: NAME/KEY: misc-feature
: OTHER INFORMATION: n=a,t,g or c
: US-09-969-708-535

```

| | | | | |
|-----------------------|-----------------|---------------|-----------|-------------|
| Query Match | 3.08; | Score 18; | DB 10; | Length 332; |
| Best Local Similarity | 100.0%; | Pred. No. 22; | | |
| Matches 18; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0 |

| | | | |
|----|-----|--------------------|-----|
| Qy | 444 | CTTGCTCCAGCCCCCACC | 461 |
| | | | |
| Db | 142 | CTTGCTCCAGCCCCCACC | 125 |

RESULT 10
US-09-918-995-565/c
: Sequence 565, Application US/09918995
: Publication No. US20030073623A1

```

? GENERAL INFORMATION:
? APPLICANT: Hyseq, Inc.
? TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
? TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
? FILE REFERENCE: 20411-756
? CURRENT APPLICATION NUMBER: US/09/918,995
? CURRENT FILING DATE: 2001-07-30
? PRIOR APPLICATION NUMBER: US/09/235,076
? PRIOR FILING DATE: 1999-01-20
? NUMBER OF SEQ ID NOS: 38054
? SOFTWARE: FASTSEQ for Windows Version 3.0
? SEQ ID NO 565
? LENGTH: 458
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1)...(458)
? OTHER INFORMATION: n = A,T,C or G
? US-09-918-995-565

```

```
Query Match      3.0%; Score 18; DB 11; Length 458;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 186 GCCACTGCTGCAGCTGCA 203
|||||
Db 118 GCCACTGCTGCAGCTGCA 101

```

RESULT 11
US-09-918-995-381/C
Sequence 381, Application US/09918995
Publication NO. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 381
LENGTH: 472
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(472)
OTHER INFORMATION: n = A,T,C or G
US-09-918-995-381

```

| | | | | |
|-----------------------|-----------------|---------------|-----------|-------------|
| Query Match | 3.0%; | Score 18; | DB 11; | Length 472; |
| Best Local Similarity | 100.0%; | Pred. No. 22; | | |
| Matches 18; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

| | | | | | | | | | | | |
|----|-----|----|----|----|----|----|----|----|----|----|-----|
| QY | 261 | GC | GG | GC | CC | CC | CA | CC | CC | CA | 278 |
| | | | | | | | | | | | |
| Db | 367 | GC | GG | GC | CC | CC | CA | CC | CC | CA | 350 |

RESULT 12
US-09-918-995-25844
Sequence 25844, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hysqg, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756


```

; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25844
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(472)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-25844
```

```

Query Match
Best Local Similarity 100.0%; Score 18; DB 11; Length 472;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

261 GCGGCGCCGCCACCCCA 278
Db 242 GCGGCGCCGCCACCCCA 259
```

```

RESULT 13
US-10-027-632-193231/C
; Sequence 193231, Application US/10027632
; GENERAL INFORMATION:
```

```

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 193231
; LENGTH: 359
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-193231
```

```

Query Match
Best Local Similarity 100.0%; Score 18; DB 13; Length 559;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

OY 100 AGGCCAACGAGGAGAT 117
Db 461 AGGCCAACGAGGAGAT 444
```

```

RESULT 14
US-10-027-632-193232/C
; Sequence 193232, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
```

```

; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 193232
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-193232
```

```

Query Match
Best Local Similarity 100.0%; Score 18; DB 13; Length 559;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

OY 100 AGGCCAACGAGGAGAT 117
Db 461 AGGCCAACGAGGAGAT 444
```

```

RESULT 15
US-10-027-632-131089/C
; Sequence 131089, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131089
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-131089
```

```

Query Match
Best Local Similarity 100.0%; Score 18; DB 13; Length 586;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

OY 321 GGCAATTAATTGCTACAG 338
Db 292 GGCAATTAATTGCTACAG 275
```

Search completed: September 25, 2003, 11:50:50
Job time : 166 secs
